

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)
10943.977 Million cell updates/sec

Perfect score: 1008
Sequence: 1 agacagactaaaaagcat.....tagataatttagaccaatgg 1008

Scoring table: IDENTITY_NUC

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

1:	gb_ba:	*
2:	gb_htg:	*
3:	gb_in:	*
4:	gb_om:	*
5:	gb_ov:	*
6:	gb_pat:	*
7:	gb_ph:	*
8:	gb_pl:	*
9:	gb_pr:	*
10:	gb_ro:	*
11:	gb_sts:	*
12:	gb_sy:	*
13:	gb_un:	*
14:	gb_vt:	*
15:	em_ba:	*
16:	em_fun:	*
17:	em_hum:	*
18:	em_in:	*
19:	em_mu:	*
20:	em_om:	*
21:	em_ov:	*
22:	em_ov:	*
23:	em_pat:	*
24:	em_ph:	*
25:	em_pl:	*
26:	em_ro:	*
27:	em_sts:	*
28:	em_un:	*
29:	em_vt:	*
30:	em_htg_hum:	*
31:	em_htg_inv:	*
32:	em_htg_mus:	*
33:	em_htg_pln:	*
34:	em_htg_rh:	*
35:	em_htg_rod:	*
36:	em_htg_mam:	*
37:	em_htg_vrt:	*
38:	em_sy:	*
39:	em_htg_hum:	*
40:	em_htg_mus:	*
41:	em_htg_other:	*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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1	1008	100.0	1008	6	AR263643	AR263643	Sequence
2	997	98.9	998	6	AX061225	AX061225	Sequence
3	981.6	97.4	1325	6	BD131596	BD131596	Secretary
4	578.4	57.4	96481	9	AC104811	AC104811	Homo sapi
5	575.2	57.1	157836	2	AC060228	AC060228	Homo sapi
6	558	55.4	639	6	BD109282	BD109282	EST and e
7	537.6	53.3	185969	2	AC069037	AC069037	Homo sapi
8	470	45.6	544	6	BD107961	BD107961	EST and e
9	460	45.6	657	6	AR263644	AR263644	Sequence
10	449	44.5	470	6	BD071746	BD071746	Secreted
11	441	41.8	450	6	BD071795	BD071795	Secreted
12	439.4	43.6	185969	2	AC069037	AC069037	Homo sapi
13	339.6	33.7	485	6	BD122986	BD122986	EST and e
14	266.4	28.4	296	6	BD071681	BD071681	Secreted
15	122.6	12.2	259038	2	AC099443	AC099443	Rattus no
16	121.2	12.0	3489	6	AR072952	AR072952	Sequence
17	121.2	12.0	3489	6	AR254713	AR254713	Sequence
18	121.2	12.0	3489	6	AR261610	AR261610	Sequence
19	121.2	12.0	3489	6	AX107938	AX107938	Sequence
20	121.2	12.0	3489	14	KSU5064	KSU5064	Sequence
21	121.2	12.0	32207	6	AR065852	AR065852	Sequence
22	121.2	12.0	32207	6	AR127850	AR127850	Sequence
23	121.2	12.0	32207	6	AR194752	AR194752	Sequence
24	121.2	12.0	137508	14	KSU76598	KSU76598	Sequence
25	117.8	11.7	28559	14	AP148805	AP148805	Kaposi's
26	115.6	11.6	1365	10	BC049645	BC049645	Mus muscu
27	115.2	11.4	133661	14	U93872	U93872	Kaposi's
28	113.2	11.2	156249	2	AL953878	AL953878	Danio rer
29	111.4	11.1	293550	2	AC094571	AC094571	Rattus no
30	111.1	11.0	177100	2	AC112388	AC112388	Rattus no
31	111	11.0	246774	2	AC095078	AC095078	Rattus no
32	110.8	11.0	2931	14	AF192756	AF192756	Kaposi's
33	110.6	11.0	5719	10	MMCATRS1	MMCATRS1	Mus muscu
34	110.6	11.0	188880	6	AC0992203	AC0992203	Mus muscu
35	110.4	11.0	2286	6	AX460942	AX460942	Sequence
36	110.4	11.0	168210	2	AC116700	AC116700	Mus muscu
37	109.6	10.9	224198	2	AC106674	AC106674	Rattus no
38	109.6	10.9	249541	2	AC095672	AC095672	Rattus no
39	109.6	10.9	249541	2	AC126196	AC126196	Rattus no
40	109.4	10.9	272545	2	AC090533	AC090533	Mus muscu
41	109	10.8	182534	10	AC074046	AC074046	Mus muscu
42	108	10.7	186559	10	AL060742	AL060742	Mouse DNA
43	108	10.7	190944	2	AC113108	AC113108	Mus muscu
44	107.8	10.7	178597	10	AL807824	AL807824	Mouse DNA
45	107.8	10.7	238518	2	AC132752	AC132752	Rattus no

ALIGNMENTS

RESULT 1				
AR263643				
LOCUS	AR263643	1008 bp	DNA	linear
DEFINITION	Sequence 1 from patent US 6331413.			
ACCESSION	AR263643			
VERSION	AR263643.1	GI:28075576		
KEYWORDS				
SOURCE	unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1008)			
TITLE	Adler,D.A. and Sheppard,P.O.			
JOURNAL	Secreted salivary Zs1G63 Polypeptide			
FEATURES	Patent: US 6331413-A 1 18-DEC-2001;			
	Location/Qualifiers			

Db	541	CAGCCACACCTGTAGACACTGAAGCTGCTGCAGAGGGGCCCTGTGTACACTAGACCTGCTG	600		
QY	606	CAGAGGCACTGTGTGAGCTGAAGCCTGTGTGCAGAGGCACTGTGTGACCTGAGCCTGTG	665		
Db	601	CAGAGGCACTGTGTGAGCTGAGCCTGTGTGCAGAGGCACTGTGTGACCTGAGCCTGTG	660		
QY	666	CAGAGGCACTGTGTGAGCTGAGCCTGTGTGCAGAGGCACTGTGTGACCTGAGCCTGTG	725		
Db	661	CAGAGGCACTGTGTGAGCTGAGCCTGTGTGCAGAGGCACTGTGTGACCTGAGCCTGTG	720		
QY	726	CAGGCAAGCCTGTGCTCCCGAGAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG	785		
Db	721	CAGGCAAGCCTGTGCTCCCGAGAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG	780		
QY	786	GAAATTCCTAGAGAGTACCAAGGCTTCATTTCTATATCTAGATGCAAAATAGTGAAT	845		
Db	781	GAAATTCCTAGAGAGTACCAAGGCTTCATTTCTATATCTAGATGCAAAATAGTGAAT	840		
QY	846	CTACAAAGTTTCTTTCTTTTCCAAAGACTATTTCAATCTGTGTATTCAGATATTC	905		
Db	841	CTACAAAGTTTCTTTCTTTTCCAAAGACTATTTCAATCTGTGTATTCAGATATTC	900		
QY	906	TCTCATCATGATGATTTGTTGTGTGTGTTTCTTCTGACCTGTAATTAATGAAAAA	965		
Db	901	TCTCATCATGATGATTTGTTGTGTGTGTTTCTTCTGACCTGTAATTAATGAAAAA	960		
QY	966	CATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1002		
Db	961	CATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	997		
RESULT 3	BD131596	1325 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD131596				
DEFINITION	Secretory proteins and polynucleotides encoding the same.				
ACCESSION	BD131596				
VERSION	BD131596.1	GI:23226541			
KEYWORDS	JP 2002503634-A/5.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (baaes 1 to 1325)				
AUTHORS	Jacobus, K., McCoy, J. M., Lavelle, E. R., Racie, L. A., Treac, M., Spaulding, V., and Agostino, M. J.				
TITLE	Secretory proteins and polynucleotides encoding the same				
JOURNAL	Patent: JP 2002503634-A 5 05-FEB-2002;				
COMMENT	GENETICS INSTITUTE INC				
	OS	Unidentified			
	PN	JP 2002503634-A/5			
	PD	05-FEB-2002			
	PF	01-JUL-1998 JP 2000501179			
	PR	02-JUL-1997 US 08/887195 27-OCT-1997 US 08/958304 PI			
	KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI				
	MAURICE TREAC,				
	PI	VIKRI SPULDING, MICHAEL J AGOSTINO			
	PC	C07K14/47, A61K38/00, A61P3/10, A61P7/00, A61P7/02, A61P7/04 PC			
		A61P7/06, A61P1/06,			
	PC	A61P17/02, A61P19/02, A61P19/04, A61P19/10, A61P21/00, A61P21/04,			
	PC	A61P25/00,			
	PC	A61P25/14, A61P25/16, A61P25/28, A61P29/00, A61P31/04, A61P31/10,			
	PC	A61P31/12,			
	PC	A61P33/00, A61P35/00, A61P35/04, A61P37/04, A61P37/06, A61P37/08,			
	PC	A61P33/00,			
	PC	C12N5/10, C12N5/09, C12P21/02, A61K39/395, A61K39/395, A61K37/02,			
	PC	C12N5/00,			
	CC	Strandedness: Double;			
	CC	Topology: linear;			
	CC	Secretory proteins and polynucleotides encoding the same FH			
Key	Location/Qualifiers				
FT	source	1..1325			
	/organism='Unidentified'.				
	Location/Qualifiers				

FEATURES

Location/Qualifiers

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Best Local Similarity	99.5%	Pred. No. 3.6e-189;			
Matches	995;	Conservative	0;	Mismatches 4;	Indels 1;
QY	10	AAAAAGCATGATTCCTTGGTCTCTCTAAAGAAAGAAATATATATTTAAAAATC	69		
DB	9	AAAAAGCATGATTCCTTGGTCTCTCTAAAGAAAGAAATATATTTAAAAATC	68		
QY	70	ATTGGATTTTCTTAACAAATTAATTAATAGTTAATATTCATAGGTCATCAAAAT	129		
DB	69	ATTGGATTTTCTTAACAAATTAATTAATAGTTAATATTCATAGGTCATCAAAAT	128		
QY	130	GAAGCTTCTCTTTGGGCTGTCATGTATGTGTGCTTTTGCAGAGAAAGACGGTCCC	189		
DB	129	GAAGCTTCTCTTTGGGCTGTCATGTATGTGTGCTTTTGCAGAGAAAGACGGTCCC	188		
QY	190	CTTCAATTGGTAGATGACATGACAGATGTCACCACTTCATTCATCTCTAAATATTC	249		
DB	189	CTTCAATTGGTAGATGACATGACAGATGTCACCACTTCATTCATCTCTAAATATTC	248		
QY	250	TTATGGCATAGGAATTTACACACCTCTCTTTATATATGAGCCAGATGAATACATCCCA	309		
DB	249	TTATGGCATAGGAATTTACACACCTCTCTTTATATATGAGCCAGATGAATACATCCCA	308		
QY	310	TTACCTTGGGAATATCTTACCTGACACAGGGTTACCTTCTGTATCCCTGATTTCTAATCTTC	369		
DB	309	TTACCTTGGGAATATCTTACCTGACACAGGGTTACCTTCTGTATCCCTGATTTCTAATCTTC	368		
QY	370	TCCTGGATTTCCCTATGCTATACATCCGCGTCTTTCCCTTAAGCTACCTCAATTGAATG	429		
DB	369	TCCTGGATTTCCCTATGCTATACATCCGCGTCTTTCCCTTAAGCTACCTCAATTGAATG	428		
QY	430	TCCTCTCTCCCTCCTTAGAGGGTTCCCGTTGTGCCCTCTTCAAGGTATTTTTCAGCAGC	489		
DB	429	TCCTCTCTCCCTCCTTAGAGGGTTCCCGTTGTGCCCTCTTCAAGGTATTTTTCAGCAGC	488		
QY	490	TGCAGCACCGCTGCCCCACCTAATTTGACGTGAGCTGTCAGCTGCACCTTTACAGC	549		
DB	489	TGCAGCACCGCTGCCCCACCTAATTTGACGTGAGCTGTCAGCTGCACCTTTACAGC	548		
QY	550	CACACCTGTAGAGCTGAGCTGCTGTCAGGGGGCCCTGTGTGACGTGAGCTGCTGTCAGC	609		
DB	549	CACACCTGTAGAGCTGAGCTGCTGTCAGGGGGCCCTGTGTGACGTGAGCTGCTGTCAGC	608		
QY	610	GGCACCTGTGAGCTGAGCTGCTGTCAGAGGCACTGTGTCAGCTGAGCCGTGTCAGC	669		
DB	609	GGCACCTGTGAGCTGAGCTGCTGTCAGAGGCACTGTGTCAGCTGAGCCGTGTCAGC	668		
QY	670	GGCACCTGTGAGCTGAGCTGTCAGAGAGAACTTACACAGCTGAGCTGCTACAGC	729		
DB	669	GGCACCTGTGAGCTGAGCTGTCAGAGAGAACTTACACAGCTGAGCTGCTACAGC	728		
QY	730	CAAGCTGCTGCCCAAGAACTCACCTTCTCTCCTTGAACAGGCAATCACTGAA	789		
DB	729	CAAGCTGCTGCCCAAGAACTCACCTTCTCTCCTTGAACAGGCAATCACTGAA	788		
QY	790	TTCTCTAAGAGATCAATGGGTCACTTTCTAATACGTATGACGAATTAAGTAAATCTAC	849		
DB	789	TTCTCTAAGAGATCAATGGGTCACTTTCTAATACGTATGACGAATTAAGTAAATCTAC	848		
QY	850	AAAAGTTTCTTCTTTTCCAAAGACTATTTCAATCTGTGTATTCAGAGTATTCATCTC	909		
DB	849	AAAAGTTTCTTCTTTTCCAAAGACTATTTCAATCTGTGTATTCAGAGTATTCATCTC	908		
QY	910	ACTACATTTGATTTGTTGTGTAGTT-TTTCCTTGGACTTAAATTAATGAAAAACAT	968		

Dn		909	ACTACATGATTGGTTTGTGGAGTTATTCCTTGCACTTAATTATATGAAAAACAAT	968
Oy		969	TGATTAATTAAATAAATAAATRGATAATTGACCATTGG	1008
Dn		969	TGATTAATTAAATAAATAAATGAATTTGACCAATGG	1008
RESULT 4				
LOCUS	AC104811		96481 bp	DNA linear PRI 16-APR-2002
DEFINITION	Homo sapiens BAC clone RP11-653L5 from 4,			complete sequence.
ACCESSION	AC104811			
VERSION	AC104811.4		GI:19698738	
KEYWORDS	HTC			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
JOURNAL	1 (bases 1 to 96481)			
MEDLINE	Sulston,J.E. and Waterston,R.			
PUBMED	Toward a complete human genome sequence			
REFERENCE	Genome Res. 8 (11), 1097-1108 (1998)			
AUTHORS	99063792			
JOURNAL	9847074			
TITLE	2 (bases 1 to 96481)			
REFERENCE	Desai,A., Haekenson,W. and Dignan,G.			
AUTHORS	The sequence of Homo sapiens BAC clone RP11-653L5			
JOURNAL	Unpublished (2001)			
REFERENCE	3 (bases 1 to 96481)			
AUTHORS	Waterston,R.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-DEC-2001) Genome Sequencing Center, Washington			
REFERENCE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
AUTHORS	MO 63108, USA			
TITLE	4 (bases 1 to 96481)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (14-MAR-2002) Genome Sequencing Center, Washington			
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
JOURNAL	MO 63108, USA			
REFERENCE	5 (bases 1 to 96481)			
AUTHORS	Waterston,R.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (24-MAR-2002) Genome Sequencing Center, Washington			
REFERENCE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
AUTHORS	MO 63108, USA			
TITLE	6 (bases 1 to 96481)			
JOURNAL	Waterston,R.H.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (29-MAR-2002) Genome Sequencing Center, Washington			
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,			
JOURNAL	MO 63108, USA			
REFERENCE	7 (bases 1 to 96481)			
AUTHORS	Waterston,R.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-APR-2002) Department of Genetics, Washington			
REFERENCE	University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA			
AUTHORS	On Mar 24, 2002 this sequence version replaced gi:19424568.			
TITLE	----- Genome Center			
JOURNAL	Center: Washington University Genome Sequencing Center			
COMMENT	Center code: WUGSC			
	Web site: http://genome.wustl.edu/gsc			
	Contact: saplen@watsn.wustl.edu			
	----- Summary Statistics			
	Center project name: H_NH0653105			

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCR-11 human BAC library was made from the blood of one male donor, as described by Ooeegawa, K., Moon, P. Y., Zhao, B., Frenken, E., Tateo, M., Catanesi, V. J., and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pletzer de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-529K3, 2000 bp overlap; the clone sequenced to the right is RP11-719M16, 2000 bp overlap. Actual end of this clone is at base position 35039 of RP11-719M16.

FEATURES

Source

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QY 319 GAATCTTACACATGACAGGGTTACCTTGGTATCCCTGATTTCTTAATTCTCTCGAATT 378
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 DB 35971 CCCCTATGTCTATCATATCTGTGTTTCCCTTACTACTAGTGAATGTTCTCTCT 36030
 QY 439 CCCTCTAGGGGTTTCCCGTTTGTCCCTCTTCAAGTTTCTTACAGAGCTGCAGACC 498
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 QY 559 AGCAGCTGAGCTGCTGTCAGAGGGCCCTGTTGACAGCTGAGCTGCTGTCAGAGCACCCTGT 618
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 QY 739 TGCCCCAGAACCTCACCCTTCTCCCTCTCTTGAACAGGCA 778
 DB 36331 TGCCCCAGAACCTCACCCTTCTCCCTCTCTTGAACAGGTA 36370

RESULT 6
 BD109282 639 bp DNA linear PAT 18-SEP-2002
 LOCUS BD109282
 DEFINITION EST and encoded human protein.
 ACCESSION BD109282.1 GI:23204100
 VERSION JP 2002010789-A/1359.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 639)
 AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
 TITLE EST and encoded human protein
 JOURNAL Patent: JP 2002010789-A 1359 15-JAN-2002;
 GENSSET CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2002010789-A/1359
 PD 15-JAN-2002
 PF 07-AUG-2000 JP 2000280989
 PR 05-AUG-1999 US 60/147499
 P1 JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
 GIORANO
 PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC
 C12N1/21,
 PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,PC
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 CC Von Heijne matrix
 CC score 10.5
 CC seq LLMWACTIVCAFA/RK
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 FT Location/Qualifiers
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 BASE COUNT 158 a 164 c 118 g 198 t 1 others

ORIGIN

Query Match 55.4%; Score 558; DB 6; Length 639;
 Best Local Similarity 99.3%; Pred. No. 4,1e-103;
 Matches 580; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 1 AGACAGACTAAAGAGCATGTATCTTGTCTCTCTTAAAGAGAGAAATATATAT 60
 DB 58 AGACAGACTAAAGAGCATGTATCTTGTCTCTCTTAAAGAGAGAAATATATAT 117
 QY 61 TAAATATACATTCGTAATTTCTTAAACAAATTAATTAATTAATTAATTAATTAAT 120
 DB 118 TAAATATACATTCGTAATTTCTTAAACAAATTAATTAATTAATTAATTAATTAAT 177
 QY 121 AATCAAAATGAACTTCTCTTGGGCTGCAATTAATTAATTAATTAATTAATTAAT 180
 DB 178 AATCAAAATGAACTTCTCTTGGGCTGCAATTAATTAATTAATTAATTAATTAAT 237
 QY 181 ACGGTTCCCTTATGAGAGATGACATGACATGACATGACATGACATGACATGACAT 240
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 DB 478 GTTGAATGTTCT 537
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 LOCUS AC069037
 DEFINITION Homo sapiens chromosome 4 clone RP11-653J5 map 4, WORKING DRAFT
 ACCESSION AC069037.1 GI:7884885
 VERSION AC069037.1
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 185969)
 AUTHORS Birren,B., Linton,L., Nuebaum,C. and Lander,E.
 JOURNAL Homo sapiens chromosome 4, clone RP11-653J5
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 185969)
 REFERENCE 2 (bases 1 to 185969)
 AUTHORS Birren,B., Linton,L., Nuebaum,C., Lander,E., Abrahams,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Baerlein,V., Beda,P.,
 Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
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 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

TITLE
JOURNAL
COMMENT

Klein, J., Labrecque, K., Lamazares, R., Landers, T., Lehoczy, J.,
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Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
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Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L7416

Center clone name: 653_L5

Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 167163 bases at least Q40

Consensus quality: 175669 bases at least Q20

Consensus quality: 179699 bases at least Q20

Insert size: 188000; agarose-fp

Insert size: 182669; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; agarose-fp

Quality coverage: 3.7 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1727: contig of 1727 bp in length
* 1728 1827: gap of 100 bp
* 1828 3423: contig of 1596 bp in length
* 3424 3523: gap of 100 bp
* 3524 6001: contig of 2478 bp in length
* 6002 6101: gap of 100 bp
* 6102 7881: contig of 1780 bp in length
* 7882 7981: gap of 100 bp
* 7982 10379: contig of 2398 bp in length
* 10380 10479: gap of 100 bp
* 10480 13080: contig of 2601 bp in length
* 13081 13180: gap of 100 bp
* 13181 15812: contig of 2632 bp in length
* 15813 15912: gap of 100 bp
* 15913 18392: contig of 2380 bp in length
* 18393 18392: gap of 100 bp
* 18393 20550: contig of 2158 bp in length
* 20551 20550: gap of 100 bp
* 20551 24116: contig of 3466 bp in length
* 24117 24216: gap of 100 bp
* 24217 27083: contig of 2867 bp in length
* 27084 27183: gap of 100 bp
* 27184 31082: contig of 3899 bp in length
* 31083 31182: gap of 100 bp
* 31183 36255: contig of 5073 bp in length
* 36256 36355: gap of 100 bp
* 36356 40430: contig of 4075 bp in length

FEATURES

source

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* 44417 44516: gap of 100 bp
* 44517 48353: contig of 3837 bp in length
* 48354 48453: gap of 100 bp
* 48454 52802: contig of 4349 bp in length
* 52803 52902: gap of 100 bp
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* 58992 59091: gap of 100 bp
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* 68028 68127: gap of 100 bp
* 68128 72911: contig of 4784 bp in length
* 72912 73011: gap of 100 bp
* 73012 79146: contig of 6135 bp in length
* 79147 79246: gap of 100 bp
* 79247 86421: contig of 7175 bp in length
* 86422 86521: gap of 100 bp
* 86522 92006: contig of 5485 bp in length
* 92007 92106: gap of 100 bp
* 92107 97911: contig of 5805 bp in length
* 97912 98011: gap of 100 bp
* 98012 103109: contig of 5098 bp in length
* 103110 103209: gap of 100 bp
* 103210 109911: contig of 6702 bp in length
* 109912 110011: gap of 100 bp
* 110012 119453: contig of 9442 bp in length
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* 119554 126958: contig of 7405 bp in length
* 126959 127058: gap of 100 bp
* 127059 134408: contig of 7350 bp in length
* 134409 134508: gap of 100 bp
* 134509 143839: contig of 9331 bp in length
* 143840 143939: gap of 100 bp
* 143940 155329: contig of 11390 bp in length
* 155330 155429: gap of 100 bp
* 155430 168024: contig of 12595 bp in length
* 168025 168124: gap of 100 bp
* 168125 185969: contig of 17845 bp in length.

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/clone_lib="RP11-11 Human Male BAC"
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/note="assembly_fragment"
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3524. 6001
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6102. 7881
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20551. 24116
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24217. 27083
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Best Local Similarity	87.6%	Pred. No. 1e-98;		
Matches 610; Conservative	0;	Mismatches 84;	Indels 2;	Gaps 2;

Dd		167408	CCAGAACCTCACCCCTTCCTCCTGTTGAACAGTAGGTGGTATATATTACTTAACCATAA	167345
Oy		803	TACCATGGCTTCATTCTCACTACTGATGCAGAATAAGCAAACTCAAAAAGTTTCTTT	862
Dd		167348	ATGTAATGGAATGAGATTTTGTAAGAGGAGAAAAAACAACACTCCCCAGCAAATCT	167289
Oy		863	CTTTTCCAAAGACTATTTTCATTCTGTGATTCAGA	898
Dd		167288	AATCAACTTAATTAATTTTTGAACAGCTTTATTCAG	167253
		RESULT 8		
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	DEFINITION	EST and encoded human protein.		
	ACCESSION	BD107961		
	VERSION	BD107961.1 GI:23202779		
	KEYWORDS	JP 2002010789-A/38.		
	SOURCE	Homo sapiens (human)		
	ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Edwards, J.B.D.M., Jobert, S. and Giordano, J.E. EST and encoded human protein Patent: JP 2002010789-A 38 15-JAN-2002;		
	REFERENCE	GENSET CORP		
	AUTHORS	OS Homo sapiens (human) PN JP 2002010789-A/38		
	TITLE	PD 15-JAN-2002 JP 2000280989 PF 07-AUG-2000 JP 2000280989 PR 05-AUG-1999 US 60/147499		
	JOURNAL	PI JEAN BABUTIST DUMAS MILNE EDWARDS, SEVEILIN JOBERT, JEAN EVE GIORDANO PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC C12N1/21, PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC C12N15/00 CC Von Heljne matrix CC score 10.5 CC seq LLMWACIVCAFA/RK FH key Location/Qualifiers FT CDS 185..544 FT sig_peptide 185..229. Location/Qualifiers 1..544 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
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	SOURCE			
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	ORIGIN			
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Qy 481 TT 482
Db 537 TT 538

RESULT 9
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DEFINITION Sequence 3 from patent US 6331413.
ACCESSION AR263644
VERSION AR263644.1 GI:28075577
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 657)
AUTHORS Adler, D.A. and Sheppard, P.O.
TITLE Secreted salivary Zsig63 Polypeptide
JOURNAL Patent: US 6331413-A 3 18-DEC-2001;
FEATURES
source 1..657
location/Qualifiers
BASE COUNT 72 a 150 c 114 g 65 t 256 others
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Best Local Similarity 61.0%; Pred. No. 3.4e-83;
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

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Qy 188 CCTTATTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 247
Db 61 CATTATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 120
Qy 248 CCTTATTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 307
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RESULT 10
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DEFINITION Secreted expressed sequence tags (ESTs).
ACCESSION BD071746
VERSION BD071746.1 GI:22617349
KEYWORDS JP 2001519667-A/556.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 470)
AUTHORS Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
TITLE Secreted expressed sequence tags (ESTs)
JOURNAL Patent: JP 2001519667-A 556 23-OCT-2001;
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location/Qualifiers
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Best Local Similarity 98.9%; Pred. No. 5.7e-81;
Matches 452; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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LOCUS BD071795 450 bp DNA linear PAT 27-AUG-2002

DEFINITION Secreterd expressed sequence tags (ESTs).

ACCESSION BD071795

VERSION BD071795.1 GI:22617398

KEYWORDS JP 2001519667-A/605.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 450)

AUTHORS Jacoby, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D., Treacy, M., Spaulding, V., and Agostino, M.J.

TITLE Secreterd expressed sequence tags (ESTs)

JOURNAL Patent: JP 2001519667-A 605 23-OCT-2001; GENETICS INSTITUTE INC

COMMENT OS Unidentified

PN JP 2001519667-A/605

PD 23-OCT-2001

PF 10-APR-1998 JP 1998543069

PR 10-APR-1997 US 08/838821

PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG.

PI MAURICE TREACY, VIRKI SPAULDING, MICHAEL J AGOSTINO PC

C12N15/12.C12N5/10.C07K14/47.C1201/68.A61K38/17 CC Strandedness: Double;

CC Topology: Linear;

CC Secreterd expressed sequence tags (ESTs)

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FT source 1.450

FT Location/Qualifiers

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BASE COUNT 112 a 113 c 78 g 147 t

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Best Local Similarity 100.0%; Pred. No. 2,8e-75;

Matches 421; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 141 TGAAGAAGAGAGCGTTCCCTTCATTTGTGAGAGTACAATGACATGATGTCACCACT 200

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Qy 349 GATATCCCTGATTTCTAATCTTCTCTGATTTCCCTATGTTATACATCCGTGTTTCC 408

Db 321 GATATCCCTGATTTCTAATCTTCTCTGATTTCCCTATGTTATACATCCGTGTTTCC 380

Qy 409 CTTAGTACTACATTTGAATGTTCTCTCTCCCTCCAGAGGGTTTCCGTTTGTCCCTCC 468

Db 381 CTTAGTACTACATTTGAATGTTCTCTCTCTCCCTCCAGAGGGTTTCCGTTTGTCCCTCC 440

Qy 469 T 469

Db 441 T 441

RESULT 12

LOCUS AC069037

DEFINITION Homo sapiens chromosome 4 clone RP11-653J5 map 4, WORKING DRAFT

ACCESSION AC069037

VERSION AC069037.1 GI:7884885

KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 185969)

AUTHORS Birren, B., Linton, L., Nuebaum, C., Landier, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barina, N., Basile, V., Bede, F., Boguslavsky, L., Boukhalter, B., Brown, A., Buckett, G., Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArliano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gege, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Hatford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margis, N., McCarthy, M., McSwan, P., McGurk, A., McKernan, K., McPherson, R., Melidrim, J., Menue, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Plesani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tassiliev, H., Vsele, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zaitoun, J., Zimmer, A. and Zody, M.

Direct Submission

TITLE Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center Code: MIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7416

```

Center clone name: 653_L-5
----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167163 bases at least Q40
Consensus quality: 175669 bases at least Q20
Consensus quality: 179699 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 182669; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1727: contig of 1727 bp in length
1728 1827: gap of 100 bp
1828 3423: contig of 1596 bp in length
3424 3523: gap of 100 bp
3524 6001: contig of 2478 bp in length
6002 6101: gap of 100 bp
6102 7881: contig of 1780 bp in length
7882 7981: gap of 100 bp
7982 10379: contig of 2398 bp in length
10380 10479: gap of 100 bp
10480 13080: contig of 2601 bp in length
13081 13180: gap of 100 bp
13181 15812: contig of 2632 bp in length
15813 15912: gap of 100 bp
15913 18292: contig of 2380 bp in length
18293 18392: gap of 100 bp
18393 20550: contig of 2158 bp in length
20551 20650: gap of 100 bp
20651 24116: contig of 3466 bp in length
24117 24216: gap of 100 bp
24217 27083: contig of 2867 bp in length
27084 27183: gap of 100 bp
27184 31082: contig of 3899 bp in length
31083 31182: gap of 100 bp
31183 36255: contig of 5073 bp in length
36256 36355: gap of 100 bp
36356 40430: contig of 4075 bp in length
40431 40530: gap of 100 bp
40531 44416: contig of 3886 bp in length
44417 44516: gap of 100 bp
44517 48353: contig of 3837 bp in length
48354 48453: gap of 100 bp
48454 52802: contig of 4349 bp in length
52803 52902: gap of 100 bp
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58992 59091: gap of 100 bp
59092 63363: contig of 4272 bp in length
63364 63463: gap of 100 bp
63464 68027: contig of 4564 bp in length
68028 68127: gap of 100 bp
68128 72911: contig of 4784 bp in length
72912 73011: gap of 100 bp
73012 79146: contig of 6135 bp in length
79147 79246: gap of 100 bp
79247 86421: contig of 7175 bp in length
86422 86521: gap of 100 bp
86522 92006: contig of 5485 bp in length
92007 92106: gap of 100 bp
92107 97911: contig of 5805 bp in length
97912 98011: gap of 100 bp
98012 103109: contig of 5098 bp in length
103110 103209: gap of 100 bp

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```

FEATURES
source
103210 109911: contig of 6702 bp in length
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119554 126958: contig of 7405 bp in length
126959 127058: gap of 100 bp
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134509 143833: contig of 9331 bp in length
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155330 155429: gap of 100 bp
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LOCUS	BD122986	485 bp	DNA	linear	PAT 18-SEP-2007
DEFINITION	EST and encoded human protein.				
ACCESSION	BD122986				
VERSION	BD122986.1	GI:23217931			
KEYWORDS	JP 2002010789-A/15063.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 485) Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.				
TITLE	EST and encoded human protein				
JOURNAL	Patent: JP 2002010789-A 15063 15-JAN-2002; GENSET CORP				
COMMENT	OS Homo sapiens (human) PN JP 2002010789-A/15063 PD 15-JAN-2002 PF 07-AUG-2000 JP 2000280989 PR 05-AUG-1999 US 60/147499 PI JEAN BAPTIST DUMAS MLNE EDWARDS,SEVELIN JOBERT,JEAN EVE GIORDANO PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC C12N1/21, PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,PC C12N15/00 CC EST and encoded human protein FH Location/Qualifiers FT source 1..485				

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QY	290	CCAGTGAATACAGTCCCGCAGTTACCCCTGGGAATCTTACACTGACACAGGGTTACCTTCG	349
Db	248	CCAGTGAATACAGTCCCGCAGTTACCCCTGGGAATCTTACACTGACACAGGGTTACCTTCG	307
QY	350	TATCCCTGGATTCTAATCTCTCGTGAATCCCTGATATGTCATATCATATCCGTGGTTTCCC	409
Db	308	TATCCCTGGATTCTAATCTCTCGTGAATCCCTGATATGTCATATCATATCCGTGGTTTCCC	367
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QY	470	TCAGAGTTTTTTAGAGAGCTGACAGACCCGCTGCCACCTATTTGACGCTGAGGCTG	527
Db	428	TTCAAGTTTTTTTACGACGCTGACAGACCCGCTGCCACCTATTTGACGCTGAGGCTG	485

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 296)	Jacobs, K., McCoy, J.M., Lavallie, E.R., Racine, L.A., Merberg, D., Treacy, M., Spaulding, V. and Agostino, M. J.	Secreted expressed sequence (ags) (ESTs)	Patent: JP 2001519667-A 491 23-OCT-2001;	GENETICS INSTITUTE INC OS Unidentified

```

PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
DAVID MERBERG
PI MAURICE TREACY, VIRKII SPALDING, MICHAEL J AGOSTINO PC
C1N1S/12.C1N5/10.C07K14/47.C1201/66.A61K38/17 CC Strandedness:
Double;
CC Topology: Linear;
CC Secretd expressed sequence tags (SESrS)
FH Key Location/Qualifiers
FT source 1..296
FT /organism='Unidentified'.

FEATURES
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Matches 287; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AC099443/
AC099443/c      259038 bp      DNA      linear      HTG 10-MAY-2003
DEFINITION      Rattus norvegicus clone CH230-197D1, *** SEQUENCING IN PROGRESS
ACCESSION      AC099443
VERSION      AC099443.5 GI:30521301
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 259038)
Muzny,D,Marie, Metzker,M, Lee, A, Abranzone, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alibrooks, S., Amin, A., Anguiano, D.,
Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Blawie, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Devalla, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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Friser, C. M., Gabisi, A., Gante, R., Garcia, A., Garner, T., Garza, M.,
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Madeshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Mundada, M., Murphy, M., Nair, L.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Worley, K.C.
Submitted (15-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259038)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:22664554.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIHL
Center clone name: CH230-197D1
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 23512 bases at least Q40
Consensus quality: 237879 bases at least Q30
Consensus quality: 240733 bases at least Q20
Estimated insert size: 249015; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 244738: contig of 244738 bp in length

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* 244739 244838: gap of unknown length
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* 246115 246214: gap of unknown length
* 246215 247343: contig of 1129 bp in length
* 247344 247443: gap of unknown length
* 247444 249475: contig of 2032 bp in length
* 249476 249575: gap of unknown length
* 249576 251459: contig of 1883 bp in length
* 251459 251558: gap of unknown length
* 251559 253388: contig of 1830 bp in length
* 253389 253488: gap of unknown length
* 253489 256838: contig of 3350 bp in length
* 256839 256938: gap of unknown length
* 256939 259038: contig of 2100 bp in length.
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FEATURES

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misc_feature

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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-197D1"
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misc_feature

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/note="wgs_end_extension"
clone_end:T7"
6380. .8323
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clone_end:T7"
9622. .10493
/note="clone_boundary"
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misc_feature

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clone_end:T7
site:Scori
```

misc_feature

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end sequence:BH321581"
38806. .33987
```

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BASE COUNT 71359 a 50156 c 50698 g 69782 t 17043 others
```

ORIGIN

Query Match

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Best Local Similarity 12.2%; Score 122.6; DB 2; Length 259038;
Matches 218; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
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```
QY 394 CATCCGCTGCTTTCCTTAGTACTCAGTGAATGTTCCCTCCCTCCTAGGGGTTT 453
Db 131745 CATCCGCTCTTTATGCTGAAGGCCAAGCAAGTGTACCAAGCATATGACAGGCGAAG 131686
QY 454 CCGGTTTGCCTCCTTCAAGGTTTTTTTTCAGACGTCGACGACCCGCTGCCCACTAT 513
Db 131685 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131626
QY 514 TGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
Db 131625 TGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131566
QY 574 TGCAGGGGGCCCTGTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633
Db 131565 TGCAGGGGGCCCTGTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131506
QY 634 TGCAGAGGCACTGTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
Db 131505 TGCAGAGGCACTGTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131446
QY 694 TGCAGAGGCACTGTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 753
Db 131445 TGCAGAGGCACTGTTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131386
QY 754 CCCTTCTCCCTCTCTTG 770
Db 131385 TCCCTGCTGCTGCTGCTG 131369
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Search completed: January 16, 2004, 08:42:23
Job time : 3777 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 05:51:13 ; Search time 336 Seconds
(without alignments)
8098.314 Million cell updates/sec

Title: US-09-923-236-1

Perfect score: 1008
Sequence: 1 agcacacacataaaagccat.....tagataatcagacacatg 1008

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1008	100.0	1008	24	AA045050	Human zsig63 DNA.
2	1008	100.0	1008	24	AB052633	DNA encoding human
3	1008	100.0	1008	24	AA020591	Human zsig63 cDNA.
4	1008	100.0	1008	25	AB033594	Human zsig63 cDNA.
5	997	98.9	998	22	AA027729	Human transport pr
6	981.6	97.4	1325	20	AA00740	Human secreted pro
7	896.4	88.9	959	20	AA01352	DNA encoding a hum
8	460	45.6	657	24	AA045051	Human zsig63 degen

9	460	45.6	657	24	AB052634	Human secreted sal
10	460	45.6	657	24	AA020592	Human zsig63 degen
11	460	45.6	657	25	AB033595	Human zsig63 degen
12	449	44.5	470	20	AA089597	EST clone CP251.
13	421	41.8	450	20	AA089646	EST clone CP116.
14	286.4	28.4	236	20	AA089532	EST clone CP128.
15	121.2	12.0	3489	21	AA030290	Kaposi's sarcoma-a
16	121.2	12.0	3489	22	AA082901	Nucleotide sequenc
17	121.2	12.0	3489	24	AB033805	Kaposi's sarcoma-a
18	121.2	12.0	32207	20	AA073805	KSHV LTR DNA (nucl
19	121.2	12.0	137507	19	AA019941	KSHV long unique c
20	106	10.5	5120	22	AA084677	DNA sequence of hu
21	100	9.9	1037	21	AA059242	Exons B, C and A o
22	100	9.9	1472	21	AA059241	Exons D, C, B and
23	99.2	9.8	1159	21	AA059240	An EcoRI fragment
24	98.2	9.7	2108	24	AB067774	Oesophagus cancer
25	93.6	9.3	397	20	AA089891	Spino cerebellar at
26	92.8	9.2	5120	22	AA084677	DNA sequence of hu
27	92.4	9.2	1101	22	AA063033	Human cDNA clone H
28	92.2	9.1	543	13	AA023092	Antigen tc-7a gene
29	89.8	8.9	877	24	AB021932	Human polynucleoti
30	89.8	8.9	3042	23	AB028445	Drosophila melanog
31	89.8	8.9	5215	23	AB028444	Drosophila melanog
32	88.4	8.8	403	21	AB010240	Trinucleotide repe
33	88.2	8.8	627	23	AA093555	DNA encoding novel
34	87.6	8.7	234	16	AA084832	Spino cerebellar at
35	87.6	8.7	1101	22	AA063033	Human cDNA clone H
36	86.6	8.6	786	17	AA046138	T. cruzi L195 homo
37	86.6	8.6	786	20	AA021097	tce coding sequenc
38	86.4	8.6	486	22	AA075507	Polyglutamine trac
39	85.2	8.5	799	19	AA055831	Nucleotide sequenc
40	85.2	8.5	1926	22	AA082902	Epsstein Barr virus
41	85.2	8.5	1926	22	AA082902	EBV tethering prot
42	85.2	8.5	2580	21	AA015454	Nucleotide sequenc
43	85.2	8.5	2580	24	AA064275	Epsstein-Barr virus
44	85.2	8.5	5452	20	AA090923	Anti-sense strand
45	85.2	8.5	8705	20	AA023778	Vector pshuttle DN

ALIGNMENTS

RESULT 1	
AA045050	AA045050 standard; DNA, 1008 BP.
ID	AA045050;
XX	AA045050;
AC	AA045050;
XX	27-DEC-2002 (first entry)
DT	27-DEC-2002 (first entry)
XX	Human zsig63 DNA.
DE	Human: secreted salivary protein; host defense protein;
XX	immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW	growth factor; cytokine; growth factor hormone activity; dental caries;
KW	infection; tooth decay; periodontal disease; gastrointestinal disease;
KW	thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KW	anti-inflammatory; chronic tissue damage; lung dysfunction; resectosis;
KW	gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW	forensic DNA profiling; chondrosarcoma; atherosclerosis; chromosome 4;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
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FT	128..172
FT	/*tag= b
FT	mat_peptide
FT	173..784
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XX US2002090677-A1.
 XX 11-JUL-2002.
 XX 03-AUG-2001; 2001US-0923236.
 XX 17-MAR-1999; 99US-124820P.
 XX 17-MAR-2000; 2000US-0527345.
 XX (ADLER/) ADLER D A.
 XX (SHEP/) SHEPPARD P O.
 XX Adler DA, Sheppard PO;
 XX WPI; 2002-642378/69.
 XX P-PSDB; AAE27862.
 XX Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
 XX agent for treating microbial infection, dental caries, periodontal
 XX disease, thrush gastrointestinal disease, and for aiding digestion
 XX
 XX Claim 3; Page 27-28; 33pp; English.

XX The invention relates to human secreted salivary polypeptide designated
 XX as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
 XX can be used in detecting agonists and antagonists of its activity, and
 XX is also useful as a host defense polypeptide, immune modulating factor,
 XX antiapathogenic polypeptide, cell-cell signalling molecule, growth factor,
 XX cytokine, or as secreted extracellular matrix associated proteins with
 XX growth factor hormone activity. It is useful for treating conditions
 XX associated with pathological microbes, including bacterial, fungal and
 XX viral infections, for treating dental caries (tooth decay), periodontal
 XX disease, thrush and gastrointestinal disease, for treating urinary tract
 XX infection, vaginal infection and for preventing infection in skin and
 XX other epithelial wounds. zsig63 is useful for establishing normal
 XX microflora and protect against pathogenic colonization and invasion, for
 XX treating chronic tissue damage e.g. damage in extremities associated
 XX with diabetes and useful as anti-inflammatory agents. It is useful as a
 XX marker of lung dysfunction, salivary gland dysfunction, or dysfunction of
 XX prostate gland. It is also therapeutically useful for aiding digestion.
 XX Polynucleotides of the invention are used in gene therapy for increasing
 XX or inhibiting zsig63 activity, for detecting abnormalities on human
 XX chromosome 4 associated with disease or other human traits and as
 XX diagnostics in forensic DNA profiling. Sequences of the invention are
 XX useful for stimulating proliferation or differentiation of cardiac
 XX myocytes, for proliferation or differentiation of adipocytes and for
 XX inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity.
 XX The present sequence is human zsig63 DNA. zsig63 gene is located on
 XX chromosome 4.
 XX
 XX Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;

Query Match 100.0%; Score 1008; DB 24; Length 1008;
 Best Local Similarity 100.0%; Pred. No. 3.5e-207;
 Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACAGACTAAAGGACATGATCTTTCGTTTCTCTAAAGAGAAAATATAAT 60
 DB 1 AGACAGACTAAAGGACATGATCTTTCGTTTCTCTAAAGAGAAAATATAAT 60
 QY 61 TAAATAATCATTTGGCTATTTTCTAAACATTAATTTATGCTTAAATTCATGGGTC 120
 DB 61 TAAATAATCATTTGGCTATTTTCTAAACATTAATTTATGCTTAAATTCATGGGTC 120
 QY 121 AATCAAAATGAAGCTTCTCTTGGGCGCATGTGATGTTGGCTTTGCAAGAGAG 180
 DB 121 AATCAAAATGAAGCTTCTCTTGGGCGCATGTGATGTTGGCTTTGCAAGAGAG 180
 QY 181 ACGGTTCCCTTCATTTGATGAGATGACATGATGATGATGATGATGATGATGAT 240
 DB 181 ACGGTTCCCTTCATTTGATGAGATGACATGATGATGATGATGATGATGATGAT 240

QY 241 GAATATTCCTTATGAGCAGATGAGAAATTTACCACTCTCTTTATTTATGCGCCAGTAATAC 300
 DB 241 GAATATTCCTTATGAGCAGATGAGAAATTTACCACTCTCTTTATTTATGCGCCAGTAATAC 300
 QY 301 AGTCCCAAGTTACCTGAGAAATACCTACACTGACACAGAGGTTACCTTGATCCCTGAT 360
 DB 301 AGTCCCAAGTTACCTGAGAAATACCTACACTGACACAGAGGTTACCTTGATCCCTGAT 360
 QY 361 TCTAACCTTCTCTGAGATTTCCCTATGTCATACATCCGAGTTTCCCTTACGATACCA 420
 DB 361 TCTAACCTTCTCTGAGATTTCCCTATGTCATACATCCGAGTTTCCCTTACGATACCA 420
 QY 421 GTTAATGTTCT 480
 DB 421 GTTAATGTTCT 480
 QY 481 TTTCAGAGCTGACAGACCCGCTGCGCCACCTATTCAGCTGAGCTGAGCTGAGCC 540
 DB 481 TTTCAGAGCTGACAGACCCGCTGCGCCACCTATTCAGCTGAGCTGAGCTGAGCC 540
 QY 541 TCTTACAGCCACACCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCC 600
 DB 541 TCTTACAGCCACACCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCC 600
 QY 601 TGCTGACAGGACCTGTTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCC 660
 DB 601 TGCTGACAGGACCTGTTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCC 660
 QY 661 TGCTGACAGGACCTGTTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCC 720
 DB 661 TGCTGACAGGACCTGTTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCC 720
 QY 721 TGCTACAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 721 TGCTACAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 781 TCAGTGAATCTCTAGAGAGTACAGAGGCTGATTTCTTACTGATGAGAAATAGT 840
 DB 781 TCAGTGAATCTCTAGAGAGTACAGAGGCTGATTTCTTACTGATGAGAAATAGT 840
 QY 841 GAAATCTACAAAGCTTCT 900
 DB 841 GAAATCTACAAAGCTTCT 900
 QY 901 ATTCACTCACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 DB 901 ATTCACTCACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 QY 961 AAAAACAATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
 DB 961 AAAAACAATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008

RESULT 2
 ID ABS52633 standard; DNA; 1008 BP.
 XX ABS52633;
 XX 15-NOV-2002 (first entry)
 XX
 XX DNA encoding human secreted salivary protein zsig63.
 XX Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
 XX antibody-cytokine; in vivo killing; pathological microbes; bacteria;
 XX fungal; viral; infection; salivary gland; anti-microbial; dental caries;
 XX tooth decay; periodontal disease; thrush; gastrointestinal disease;
 XX urinary tract infection; vaginal infection; skin infection; microflora;
 XX epithelial wound; pathogenic colonization; invasion; pro-inflammatory;
 XX chronic tissue damage; vascular system; diabetes; anti-inflammatory;
 XX incompetent immune system; AIDS; acquired immunodeficiency syndrome;
 XX chemotherapy; radiation treatment; lung infection; cystic fibrosis;
 XX digestion; chromosome 4; gene; de.

XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 128..787
 FT /tag= a
 FT /product= "Human secreted salivary protein zsig63"
 FT misc_feature 128..784
 FT /tag= b
 FT /note= "Specifically claimed in claim 3"
 FT misc_feature 173..784
 FT /tag= c
 FT /note= "Specifically claimed in claim 3"
 XX US2002081701-A1.
 XX 27-JUN-2002.
 XX 03-AUG-2001; 2001US-0922480.
 XX 17-MAR-1999; 99US-124820P.
 XX 17-MAR-2000; 2000US-0527345.
 XX (ADLER/) ADLER D A.
 XX (SHEP/) SHEPPARD P O.
 XX Adler DA, Sheppard PO;
 XX WPI: 2002-635468/68.
 XX P-PSDB; ABG31608.
 XX Novel secreted salivary protein, zsig63 and polynucleotide encoding it
 XX useful for treating microbial infections, inflammatory conditions,
 XX dental caries and lung infections associated with cystic fibrosis
 XX
 XX Claim 3; Page 27-28; 33pp; English.
 XX
 XX The present invention relates to a new secreted salivary protein, zsig63.
 XX The invention is useful for detecting in a test sample, the presence of
 XX an antigenist or agonist of zsig63 protein activity. The invention is
 XX also useful as an immunogen for producing an antibody to zsig63
 XX polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
 XX protein are useful for enhancing in vivo killing of target tissues.
 XX Pharmaceutical composition comprising purified zsig63 polypeptide are
 XX useful in the treatment of conditions associated with pathological
 XX microbes, including bacterial, fungal and viral infections. High
 XX expression of zsig63 in salivary gland suggests that anti-microbial
 XX polypeptides are useful for treatment of dental caries ('tooth decay'),
 XX periodontal disease, thrush and gastrointestinal disease. Other
 XX applications can be used in urinary tract infections, vaginal infections,
 XX prevention of infection in skin and other epithelial wounds. The
 XX polypeptides can be used to establish normal microflora and protect
 XX against pathogenic colonisation and invasion. The invention is useful
 XX when pro-inflammatory activity is desired. Applications for
 XX such pro-inflammatory activity include the treatment of chronic tissue
 XX damage, particularly in areas having a limited or damaged vascular system
 XX e.g., damage in extremities associated with diabetes. Antagonists to
 XX zsig63 polypeptides may be useful as anti-inflammatory agents. The
 XX invention is useful for the treatment of patients having incompetent
 XX immune system, such as AIDS (acquired immunodeficiency syndrome) patients
 XX or individuals that have undergone chemotherapy, radiation treatment. The
 XX invention is also useful for the treatment of lung infections associated
 XX with cystic fibrosis and its agonists or antagonists are useful for
 XX aiding digestion. The present nucleic acid sequence represents the human
 XX zsig63 gene located on chromosome 4. This sequence encodes the human
 XX secreted salivary protein zsig63 of the invention.
 XX
 XX Sequence 1008 BP, 257 A, 251 C, 193 G, 307 T, 0 other;
 XX
 XX Query Match 100.0%; Score 1008; DB 24; Length 1008;
 XX Best Local Similarity 100.0%; Pred. No. 3.5e-207;
 XX Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGACAGACTAAAAAGCCATGATTTCTTGCTTCTCTTAAAAAGAAAAATATATTT 60
 Db 1 AGACAGACTAAAAAGCCATGATTTCTTGCTTCTCTTAAAAAGAAAAATATATTT 60
 Qy 61 TAAATATACATTCGATTTCTTAAAAAATATATATATATATATATATATATATAT 120
 Db 61 TAAATATACATTCGATTTCTTAAAAAATATATATATATATATATATATATATAT 120
 Qy 121 AATCAAAATGAAGTTTCTTTGGGCTGATTTGATTTGTTGCTTTGCAAGAGAG 180
 Db 121 AATCAAAATGAAGTTTCTTTGGGCTGATTTGATTTGTTGCTTTGCAAGAGAG 180
 Qy 181 ACGGTTCCCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 ACGGTTCCCTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Qy 241 GAATATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Db 241 GAATATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Qy 301 AGTCCCAAGTTACCTTGGGAATCTTACCTGACAGAGGTTACCTTCCCTGAT 360
 Db 301 AGTCCCAAGTTACCTTGGGAATCTTACCTGACAGAGGTTACCTTCCCTGAT 360
 Qy 361 TCTAATCTTCTGATGATTTCCCTATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 TCTAATCTTCTGATGATTTCCCTATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 421 GTTGAATGTTCT 480
 Db 421 GTTGAATGTTCT 480
 Qy 481 TTGACAGCTGACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 481 TTGACAGCTGACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Qy 541 TCTTACAGCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 541 TCTTACAGCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Qy 601 TGTGCAAGAGCACTGTTGAGCTGAGCTGCAAGAGCACTGTTGAGCTGAGCC 660
 Db 601 TGTGCAAGAGCACTGTTGAGCTGAGCTGCAAGAGCACTGTTGAGCTGAGCC 660
 Qy 661 TGTGCAAGAGCACTGTTGAGCTGAGCTGCAAGAGCACTGTTGAGCTGAGCC 720
 Db 661 TGTGCAAGAGCACTGTTGAGCTGAGCTGCAAGAGCACTGTTGAGCTGAGCC 720
 Qy 721 TGTACAGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Db 721 TGTACAGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Qy 781 TCAAGTAAATTTCTAGAGAGTACATGAGTATTTCTATTTCTATGATGAGAAATAGT 840
 Db 781 TCAAGTAAATTTCTAGAGAGTACATGAGTATTTCTATTTCTATGATGAGAAATAGT 840
 Qy 841 GAAATCTACAAAGTTTCTTTCTTTTCAAAAGCTATTTATTTCTGTTATTCAGAGT 900
 Db 841 GAAATCTACAAAGTTTCTTTCTTTTCAAAAGCTATTTATTTCTGTTATTCAGAGT 900
 Qy 901 ATTATCTCACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 Db 901 ATTATCTCACTACATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 Qy 961 AAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008
 Db 961 AAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008
 XX
 XX RESULT 3
 XX AAS20591
 XX ID AAS20591 standard; cDNA, 1008 BP.

AA520591;
 23-APR-2002 (first entry)
 Human zsig63 cDNA.
 Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss; microbial infection; tooth decay; periodontal disease; thrush; emphysema; gastrointestinal disease; urinary tract infection; vaginal infection; skin infection; epithelial wound; chronic tissue damage; cystic fibrosis; acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis; chronic bronchitis; gene therapy; protein therapy; gene.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 128..787
 /tag= a
 /product= "Human zsig63"
 US6331413-B1.
 18-DEC-2001.
 17-MAR-2000; 2000US-0527345.
 17-MAR-1999; 99US-124820P.
 (ZYMO) ZYMOGENETICS INC.
 Adler DA, Sheppard PO;
 WPI; 2002-096707/13.
 P-PSDB; AAU74536.
 Polynucleotides encoding salivary proteins useful as anti-microbial agents -
 Claim 2; Column 47-50; 29pp; English.
 The invention relates to a polynucleotide derived from the 4q12-4q13 region of human chromosome 4 and encoding a zsig63 polypeptide, a secreted salivary protein with anti-microbial activity. Due to their microbial activity, the sequences can be used in the study of microbial infections, e.g. for recombinant production of anti-microbial proteins. The sequences can be used in the treatment of tooth decay, periodontal disease, thrush, gastrointestinal disease, urinary tract infections, vaginal infections, skin infections, epithelial wounds, chronic tissue damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung infections, sarcoidosis, emphysema and chronic bronchitis. This sequence represents cDNA encoding human zsig63.
 Sequence 1008 BP; 257 A; 251 C; 193 G; 307 T; 0 other;
 Query Match 100.0%; Score 1008; DB 24; Length 1008;
 Best Local Similarity 100.0%; Pred. No. 3.5e-207;
 Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

241 GAATATTCCTTAATGGCATACAGGAATTTACACCTCTCTTTATATGCGCCAGTGAATAC 300
 241 GAATATTCCTTAATGGCATACAGGAATTTACACCTCTCTTTATATGCGCCAGTGAATAC 300
 301 AGTCCCAAGTTACCTGGGAATACTTAACCTGACAGAGGTTACCTTGATCCCTGGAT 360
 301 AGTCCCAAGTTACCTGGGAATACTTAACCTGACAGAGGTTACCTTGATCCCTGGAT 360
 361 TCTAATCTTCTGGAATTCCTTATGCTATACATACCGGTTTCCCTTAAGTACTCA 420
 361 TCTAATCTTCTGGAATTCCTTATGCTATACATACCGGTTTCCCTTAAGTACTCA 420
 421 GTGAATGTCCTCTCTCCCTCTAGGGGTTTCCGTTTTCCTCTCAAGTTT 480
 421 GTGAATGTCCTCTCTCCCTCTAGGGGTTTCCGTTTTCCTCTCAAGTTT 480
 481 TTCAGCAGCTGACAGCCCGCTGCCCCACCTATTGACAGCTGAGCTGCTGAC 540
 481 TTCAGCAGCTGACAGCCCGCTGCCCCACCTATTGACAGCTGAGCTGCTGAC 540
 541 TCTTACAGCCACCTGTTAGAGCTGAGCTGCTGAGGGGCTGTTGAGCTGAGCC 600
 541 TCTTACAGCCACCTGTTAGAGCTGAGCTGCTGAGGGGCTGTTGAGCTGAGCC 600
 601 TGCTGAGAGGCACTGTTGAGCTGAGCTGAGCTGAGGGGCTGTTGAGCTGAGCC 660
 601 TGCTGAGAGGCACTGTTGAGCTGAGCTGAGCTGAGGGGCTGTTGAGCTGAGCC 660
 661 TGCTGAGAGGCACTGTTGAGCTGAGCTGAGCTGAGGGGCTGTTGAGCTGAGCC 720
 661 TGCTGAGAGGCACTGTTGAGCTGAGCTGAGCTGAGGGGCTGTTGAGCTGAGCC 720
 721 TGCTACAGCCCAAGCTGCTGCCCCAGAACCTTCTCTCTGTTGAGCAAGCAAA 780
 721 TGCTACAGCCCAAGCTGCTGCCCCAGAACCTTCTCTCTGTTGAGCAAGCAAA 780
 781 TCAGTGAATCTCTAGAGAGTACATGAGGTTCTTCTACTGATGCAAGTAATAGT 840
 781 TCAGTGAATCTCTAGAGAGTACATGAGGTTCTTCTACTGATGCAAGTAATAGT 840
 841 GAATCTACAAAGTTTCTTCTTCCAAAGACTATTTGATTCAGAGT 900
 841 GAATCTACAAAGTTTCTTCTTCCAAAGACTATTTGATTCAGAGT 900
 901 ATTCACTCACTACATGATTTGTTGGTGGTATTTCTTGAATTAATTAATGA 960
 901 ATTCACTCACTACATGATTTGTTGGTGGTATTTCTTGAATTAATTAATGA 960
 961 AAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATGA 1008
 961 AAAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATGA 1008
 RESULT 4
 ABX93594
 ID ABX93594 standard; cDNA, 1008 BP.
 ABX93594;
 28-MAY-2003 (first entry)
 Human cDNA encoding zsig63.
 Human; ss; gene; zsig63; adhesion; salivary gland; dental caries; periodontal disease; thrush; gastrointestinal disease; epithelial wound; urinary tract infection; vaginal infection; skin infection; pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS; lung infection; cystic fibrosis; lung dysfunction; digestive; salivary gland carcinoma; pneumocystis carinii infection; emphysema; chronic bronchitis; prostate dysfunction; prostate adenocarcinoma; cell culture media; gene therapy; human chromosome 4q12-4q13; dentinogenesis imperfecta; dentin dysplasia type II.

XX	Homo sapiens.
XX	
XX	Location/Qualifiers
XX	Key CDS
FT	128..787
FT	/tag= a
FT	/product= "zsig63"
FT	/note= "This CDS (minus the stop codon) is claimed in claim 3"
FT	claim 3"
FT	128..172
FT	/tag= b
FT	173..784
FT	/tag= c
FT	/label= Mature_zsig63
FT	/note= "This region is claimed in claim 3"
PX	US2002173027-A1.
PD	21-NOV-2002.
XX	
XX	03-AUG-2001; 2001US-0922469.
PF	
PR	17-MAR-1999; 99US-124820P.
PR	17-MAR-2000; 2000US-0527345.
PA	(ADLER/) ADLER D A.
PA	(SHEP/) SHEPPARD P O.
PI	Adler DA, Shepard PO;
XX	
XX	WPI; 2003-328428/31.
DR	P-PSDB; ABU08515.
XX	
PT	Novel isolated zsig63 polypeptide, member of the adhesin family, useful
PT	for treating dental caries, periodontal disease, thrush,
PT	gastrointestinal disease, urinary tract infections, vaginal infections,
PT	skin infections -
PS	
XX	Claim 3; Page 26-27; 32pp; English.
CC	The invention relates to an isolated zsig63 polypeptide comprising at least 90% identity to an amino acid sequence which comprises domain 1 of zsig63, domain 2, domain 3, mature zsig63 and full length zsig63. Also included are the polynucleotide encoding zsig63, a zsig63 expression vector, a cultured cell comprising the vector and expressing the protein, a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-126, 127-219 or 16-219 of zsig63 and an additional protein), using a zsig63 reporter gene construct to identify zsig63 agonists, and producing an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is useful for detecting in a test sample, the presence of antagonist of zsig63 protein activity. zsig63 has antimicrobial activity and since exhibits high expression in salivary gland, can be used for treating dental caries, periodontal disease, thrush, and gastrointestinal disease, urinary tract infections, vaginal infections, skin infections and other epithelial wounds. The polypeptides can be used to establish normal microflora and protect against pathogenic colonization and invasion. Zsig63 can also be used for providing pro-inflammatory activity for treating chronic, tissue damage particularly in areas having limited or damaged vascular system, e.g. in diabetes, and for treating immuno-compromised AIDS patients or in individuals that have undergone chemotherapy, radiation treatment, for treating lung infections e.g. in cystic fibrosis. Detection of zsig63 polypeptide at relatively high levels in the trachea may indicate that such polypeptides may serve as a marker of lung dysfunction. Zsig63 is also useful in diagnosing conditions associated with salivary gland or lung dysfunction including salivary gland carcinoma, Pneumocystis carinii infection, emphysema, chronic bronchitis, prostate dysfunctions such as prostate adenocarcinoma, aiding digestion, and as components of defined cell culture media and may be used to replace serum that is commonly used in culture. The DNA is useful in gene therapy applications to increase or inhibit zsig63 activity, and for detecting abnormalities on human chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta, and dentin dysplasia type II). zsig63 is an adhesin family


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FT      /tag= a
FT      /product= "secreted protein clone cpl16 1"
XX      MO9901466-A1.
XX      PD 14-JAN-1999.
XX      PE 01-JUL-1998; 98MO-US13813.
XX      PR 27-OCT-1997; 97US-0958304.
XX      PR 02-JUL-1997; 97US-0887195.
XX      PA (GEMV ) GENETICS INST INC.
PI      Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Racine LA;
PI      Spaulding V, Treacy M;
DR      WPI; 1999-105994/09.
DR      P-PDSB; AAM30653.
XX      New polynucleotides encoding secreted human proteins - are derived
XX      from human foetal brain, adult testes, adult brain, foetal kidney,
XX      adult salivary gland, or adult blood cDNA libraries, useful as, e.g.
XX      potential vaccines
PS      Claim 23; Page 70-71; 107pp; English.
XX
XX      The present sequence encodes a human secreted protein from clone
CC      cpl16 1, deposited as ATCC 98482. Human secreted protein clone
CC      polynucleotides and proteins are predicted to have biological
CC      activities which would make them suitable for treating, preventing or
CC      ameliorating medical conditions in humans and animals. Suggested
CC      activities include nutritional activity, cytokine and cell
CC      proliferation/differentiation activity, immune stimulating (e.g. as
CC      vaccines) or suppressing activity, haematopoiesis regulating activity,
CC      tissue growth activity, activin/inhibin activity, chemotactic/
CC      chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC      ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC      suppressor activity, and tumour inhibition activity. The polynucleotides
CC      are also stated to be useful for gene therapy.
SQ      Sequence 1325 BP; 407 A; 289 C; 241 G; 388 T; 0 other;
Query Match          97.4%; Score 961.6; DB 20; Length 1325;
Best Local Similarity 99.5%; Pred. No. 1.9e-201;
Matches 995; Conservative 0; Mismatches 4; Indels 1; Gaps 1,
QY      10 AAAAAAGCATATTCCTTTGGTCTCTCTCAAAAGAAGAAAATATTAATTTAAAAATAC 69
DB      9 AAAAAAGCATATTCCTTTGGTCTCTCTCAAAAGAAGAAAATATTAATTTAAAAATAC 68
QY      ATTGGATTATTTCTAAACAATAAATTAATAGTGTTAATATTCATAGGGTCAATCAAAAT 129
DB      69 ATTGGATTATTTCTAAACAATAAATTAATAGTGTTAATATTCATAGGGTCAATCAAAAT 128
QY      130 GAAGCTTCCTTTGGGCGCTGCATTGTATGTGTTCCTTTGGCAAGGAAGAGCGGTTCC 189
DB      129 GAAGCTTCCTTTGGGCGCTGCATTGTATGTGTTCCTTTGGCAAGGAAGAGCGGTTCC 188
QY      190 CTTCATTGTGAGATGACATGACATGACATGACATGCCACTTCATCCTCGAATATTC 249
DB      189 CTTCATTGTGAGATGACATGACATGACATGACATGCCACTTCATCCTCGAATATTC 248
QY      250 TTATGGCATTAGGAAATTTACACACCTCCTTTATATATGAGCCAGAGAAATACAGTCCGAG 309
DB      249 TTATGGCATTAGGAAATTTACACACCTCCTTTATATATGAGCCAGAGAAATACAGTCCGAG 308
QY      310 TTACCCTGGGAATACTTACACTGACACAGGGTTACCTTCGATATCCCTGGATTCTAACCTTC 369
DB      309 TTACCCTGGGAATACTTACACTGACACAGGGTTACCTTCGATATCCCTGGATTCTAACCTTC 368
QY      370 TCCCGAATCCCCTATGCTATCAATCCGAGTTTTCCCTTAGTACTCACTGAATGAT 429

```

Db	369	TCCTGGATTCCCTCTATGCTATACATCCGCGTGTTCCTTCCCTTAGCTACGTAGTGAATGT	428
Qy	430	TCCTCTCTCCCTCTCTAGGAGGTTTCCCGTTGTCTCCCTCAAGTTTTTTTTCAGCAGC	489
Db	429	TCCTCTCTCCCTCTAGGAGGTTTCCCGTTGTCTCCCTCAAGTTTTTTTTCAGCAGC	488
Qy	430	TGCAGACCCGCTGCCCCACCTATTTGAGCTGAGCGCTGTGAGCTGCACCTCTTACAGC	549
Db	489	TGCAGACCCGCTGCCCCACCTATTTGAGCTGAGCGCTGTGAGCTGCACCTCTTACATC	548
Qy	550	CACACCTGTAGCAGCTGAGCCTGTCTGACGAGGCCCCCTGTGTGAGCTGAGCCTGTCCAGA	609
Db	549	CACACCTGTAGATTTGAGCCTGTCTGACGAGGCCCCCTGTGTGAGCTGAGCCTGTCCAGA	608
Qy	610	GGCACCTGTGTGAGCTGAGCCTGTCTGACAGGCGACCTGTGTGAGCTGAGCCTGTCCAGA	669
Db	609	GGCACCTGTGTGAGCTGAGCCTGTCTGACAGGCGACCTGTGTGAGCTGAGCCTGTCCAGA	668
Qy	670	GGCACCTGTGTGAGCTGAGCCTGTCTGACAGGCGACCTGTGTGAGCTGAGCCTGTCCAGC	729
Db	669	GGCACCTGTGTGAGCTGAGCCTGTCTGACAGGCGACCTGTGTGAGCTGAGCCTGTCCAGC	728
Qy	720	CAAGCCTCTGCCCCCAGAACCTCAACCTTCTCCCTCTCTTGAACAGGCAAAATCAGTAAA	789
Db	729	CAAGCCTCTGCCCCCAGAACCTCAACCTTCTCCCTCTCTTGAACAGGCAAAATCAGTAAA	788
Qy	790	TTCTCTAGAAGAGTACCATGGGTTTCATTTCTATCTGATGTCAGAAATTAAGTAAATCTAC	849
Db	789	TTCTCTAGAAGAGTACCATGGGTTTCATTTCTATCTGATGTCAGAAATTAAGTAAATCTAC	848
Qy	850	AAAAATTTTCTTTCTTTTCCAAAGCTATTTCTATCTGTGTATTCAGAGTATTCATCTC	909
Db	849	AAAAATTTTCTTTCTTTTCCAAAGCTATTTCTATCTGTGTATTCAGAGTATTCATCTC	908
Qy	910	ACTACATGATTTGTTGTGNGTAGTT-TTCCCTTGGACTTAATTTATATTTGAAAAAATCAT	968
Db	909	ACTACATGATTTGTTGTGNGTAGTTTCTTGGACTTAATTTATATTTGAAAAAATCAT	968
Qy	969	TGATTAATTAATTAATAAATAGATTAATTTAGACCAATGG	1008
Db	969	TGATTAATTAATTAATAAATAGATTAATTTAGACCAATGG	1008
RESULT 7			
AAx61352			
ID	AAx61352	standard; cDNA; 959 BP.	
AC	AAx61352;		
DT	14-JUL-1999	(first entry)	
XX			
DE	DNA encoding a human secreted protein.		
XX			
KM	Human secreted protein; cancer; tumour; neurodegenerative disorder;		
KM	developmental abnormality; fetal deficiency; blood disorder; leukemia;		
KM	immune system disease; autoimmune disease; hepatic disease;		
KM	renal disease; lymphoma; inflammation; allergy; ischemic shock;		
KM	Alzheimer's; cognitive disorder; schizophrenia; prostate disease;		
KM	obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;		
KM	lung disease; thymus disease; digestive disorder; endocrine disorder;		
XX			
OS	Homo sapiens.		
XX			
PN	W09922243-A1.		
XX			
PD	06-MAY-1999.		
XX			
PF	23-OCT-1998;	98WO-US22376.	
XX			
PR	24-OCT-1997;	97US-0063387.	
PR	24-OCT-1997;	97US-0062784.	
PR	24-OCT-1997;	97US-0063088.	

PR 24-OCT-1997; 97US-0063089.
 PR 24-OCT-1997; 97US-0063090.
 PR 24-OCT-1997; 97US-0063091.
 PR 24-OCT-1997; 97US-0063092.
 PR 24-OCT-1997; 97US-0063097.
 PR 24-OCT-1997; 97US-0063098.
 PR 24-OCT-1997; 97US-0063099.
 PR 24-OCT-1997; 97US-0063100.
 PR 24-OCT-1997; 97US-0063101.
 PR 24-OCT-1997; 97US-0063109.
 PR 24-OCT-1997; 97US-0063110.
 PR 24-OCT-1997; 97US-0063111.
 PR 24-OCT-1997; 97US-0063148.
 PR 24-OCT-1997; 97US-0063386.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Brewer LA, Carter KC, Duan DR, Ebner R, Endress GA;
 PI Feng P, Florence C, Florence KA, Greene JM, Janat F;
 PI Kaye H, Lafleur DW, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Wei Y, Young P;
 XX MPI; 1999-303069/25.
 DR P-PSDB; AAY19472.
 XX
 PT New isolated human genes and the secreted polypeptides they encode
 XX
 PS Claim 3; Page 328-329; 546pp; English.
 XX
 CC The specification describes cDNA sequences (AAX61322-X61470) encoding
 CC human secreted proteins (AAY19442-Y19590). The polynucleotides and their
 CC corresponding secreted polypeptides are useful for preventing, treating
 CC or ameliorating medical conditions, e.g. by protein or gene therapy.
 CC Pathological conditions can also be diagnosed by determining the amount
 CC of the polypeptides in a sample or by determining the presence of
 CC mutations in the polynucleotides. Specific uses are described for each
 CC of the polynucleotides, based on which tissues they are most highly
 CC expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, neurodegenerative disorders, developmental
 CC abnormalities and fetal deficiencies, blood disorders, leukemias,
 CC diseases of the immune system, autoimmune diseases, hepatic and renal
 CC diseases, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, prostate diseases, obesity,
 CC disorders involving osteoclasts such as osteoporosis, arthritis or
 CC malignancies, diseases of testes, lung or thymus, digestive/endorine
 CC disorders, infections and AIDS. The polypeptides are also useful for
 CC identifying their binding partners.
 CC
 XX
 SQ Sequence 959 BP; 240 A; 245 C; 187 G; 286 T; 1 other;
 Query Match 88.9%; Score 896.4; DB 20; Length 959;
 Best Local Similarity 98.8%; Pred. No. 3.5e-183;
 Matches 923; Conservative 1; Mismatches 7; Indels 3; Gaps 2;
 QY 75 GATTTTCTAAAGCATTAATTATAGTGAATATTCATAGGCGCATCAAAATGAAGC 134
 DB 12 GATTTTCTAAAGCATTAATTATAGTGAATATTCATAGGCGCATCAAAATGAAGC 71
 QY 135 TTCTCTTTGGGCGCTGCATTTGATGTGTGCTTTTGAAGAAGAGAGGTTCCCTTCA 194
 DB 72 TTCTCTTTGGGCGCTGCATTTGATGTGTGCTTTTGAAGAAGAGAGGTTCCCTTCA 131
 QY 195 TTGGTGAAGATGACATGACATGATGTGTGCTTCCATTCATCTCTGAATATTTCTTATG 254
 DB 132 TTGGTGAAGATGACATGACATGATGTGTGCTTCCATTCATCTCTGAATATTTCTTATG 191
 QY 255 GCATCGGAATTTACACCTCTCTTTATATGCGCCAGTAATACAGTCCCACTTAC 314
 DB 192 GCATCGGAATTTACACCTCTCTTTATATGCGCCAGTAATACAGTCCCACTTAC 251
 QY 315 CTGGGAATATCTTACATGACAGAGGTTACCTTCTGATCCCTGATTTCAATCTTCTCTG 374
 DB 252 CTGGGAATATCTTACATGACAGAGGTTACCTTCTGATCCCTGATTTCAATCTTCTCTG 311

QY 375 GATTCCTATGATCTATACATCCGNGTTTTCCCTTAGACTACAGTTGAATGTCCTC 434
 DB 312 GATTCCTATGATCTATACATCCGNGTTTTCCCTTAGACTACAGTTGAATGTCCTC 371
 QY 435 CTCTCCCTCTTAAGGGGTTTCCGTTTGTCTCTCTTCAAGTTTCTTTCAGACAGTGCAG 494
 DB 372 CTCTCCCTCTTAAGGGGTTTCCGTTTGTCTCTCTTCAAGTTTCTTTCAGACAGTGCAG 431
 QY 495 CACCGCTGCCCCACCTATTTGACAGCTGAGCTGCTGACAGTGCACCTCTTACAGCCAC 554
 DB 432 CACCGCTGCCCCACCTATTTGACAGCTGAGCTGCTGACAGTGCACCTCTTACAGCCAC 491
 QY 555 CTGTAGACAGCTGAGCCCTGCTGAGAGGCGCCCTGTGTGACAGCTGAGCCCTGCTGAG 612
 DB 492 CTGTAGACAGCTGAGCCCTGCTGAGAGGCGCCCTGTGTGACAGCTGAGCCCTGCTGAG 551
 QY 613 ACCTGTTGAGC-TGAGCCTGCTGACAGAGGACCTGTTGACAGCTGAGCTGCTGACAGG 671
 DB 552 ACCTGTTGAGCTTGAAGCTGCTGCTGACAGAGGACCTGTTGACAGCTGAGCTGCTGACAGG 611
 QY 672 CACCTGTTGAGTGAAGCAGCTGCTGACAGAGAACCTTCAACAGCTGAGCTGCTTACAGCA 731
 DB 612 CACCTGTTGAGTGAAGCAGCTGCTGACAGAGAACCTTCAACAGCTGAGCTGCTTACAGCA 671
 QY 732 AGCTGCTGCCCCGAGAACCTTCAACCTTCTCTCTCTTGTGAACAGGCAAAATGAGAAAT 791
 DB 672 AGCTGCTGCCCCGAGAACCTTCAACCTTCTCTCTCTTGTGAACAGGCAAAATGAGAAAT 731
 QY 792 CTCTAGAAGATGACATGAGGTTCAATTTCTATCTAGTACAGAAATAGTAAATCTACAA 851
 DB 732 CTCTAGAAGATGACATGAGGTTCAATTTCTATCTAGTACAGAAATAGTAAATCTACAA 791
 QY 852 AAGTTTCTTTCTTTTCCAAAGACTATTCTCTGTGTATTCAGAGTATTCATCTCAC 911
 DB 792 AAGTTTCTTTCTTTTCCAAAGACTATTCTCTGTGTATTCAGAGTATTCATCTCAC 851
 QY 912 TACATTTATTTTGTGTGATGTTTCTTCTGAGCTTAATTTATGAAAAAATTTGA 971
 DB 852 TACATTTATTTTGTGTGATGTTTCTTCTGAGCTTAATTTATGAAAAAATTTGA 911
 QY 972 TAATTAATAATAATAATAGATAATTTAGACCAA 1005
 DB 912 TAATTAATAATAATAATAGATAATTTAGACCAA 945
 RESULT 8
 AAD45051
 ID AAD45051 standard; DNA; 657 BP.
 XX
 AC AAD45051;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human zslg63 degenerate DNA.
 XX
 KW Human; secreted salivary protein; zslg63 protein; host defense protein;
 KW immune modulating factor; antipathogenic; cell-cell signalling molecule;
 KW growth factor; cytokine; growth factor hormone activity; dental caries;
 KW infection; tooth decay; periodontal disease; gastrointestinal disease;
 KW thrush; urinary tract infection; vaginal infection; diabetes; obesity;
 KW anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
 KW gene therapy; salivary gland dysfunction; prostate gland dysfunction;
 KW forensic DNA profiling; chondrosarcoma; atherosclerosis; chromosome 4;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 FN US2002090677-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 03-AUG-2001; 2001US-0923236.

PS Claim 4; Page 28-29; 33pp; English.

XX The present invention relates to a new secreted salivary protein, zsig63.
 CC The invention is useful for detecting in a test sample, the presence of
 CC an antagonist or agonist of zsig63 protein activity. The invention is
 CC also useful as an immunogen for producing an antibody to zsig63
 CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
 CC proteins are useful for enhancing in vivo killing of target tissues.
 CC Pharmaceutical composition comprising purified zsig63 polypeptide are
 CC useful in the treatment of conditions associated with pathological
 CC microbes, including bacterial, fungal and viral infections. High
 CC expression of zsig63 in salivary gland suggests that anti-microbial
 CC polypeptides are useful for treatment of dental caries (tooth decay),
 CC periodontal disease, thrush and gastrointestinal disease. Other
 CC applications can be used in urinary tract infections, vaginal infections,
 CC prevention of infection in skin and other epithelial wounds. The
 CC polypeptides can be used to establish normal microflora and protect
 CC against pathogenic colonisation and invasion. The invention is useful
 CC when pro-inflammatory activity is desired. Applications for
 CC such pro-inflammatory activity include the treatment of chronic tissue
 CC damage, particularly in areas having a limited or damaged vascular system
 CC e.g., damage in extremities associated with diabetes. Antagonists to
 CC zsig63 polypeptides may be useful as anti-inflammatory agents. The
 CC invention is useful for the treatment of patients having incompetent
 CC immune system, such as AIDS (acquired immunodeficiency syndrome) patients
 CC or individuals that have undergone chemotherapy, radiation treatment. The
 CC invention is also useful for the treatment of lung infections associated
 CC with cystic fibrosis and its agonists or antagonists are useful for
 CC aiding digestion. The present nucleic acid sequence encodes the human
 CC secreted salivary protein zsig63 of the invention.

XX Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;

Query Match 45.6%; Score 460; DB 24; Length 657;
 Best Local Similarity 61.0%; Pred. No. 2.2e-89;
 Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

OY 128 ATGAAGCTTCCTCTGGGCGCTGATGATGTTGCTTTGGCAAGAGAGCGGTTTC 187
 DB 1 ATGAARNTNTNTTGTGGCMTGATGHTGTGTGTCGTCMGAARAGNNAGNTTY 60
 OY 188 CCTTCATTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
 DB 61 CCTTTATHTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 OY 248 CCTTATGCGATACGGAATTTACCACTCTCTTTATATCGCCAGTGAATACGTTCCC 307
 DB 121 CATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 OY 308 AGTTACCTGGGATATCTTACATGATGATGATGATGATGATGATGATGATGATGAT 367
 DB 181 WSNATYCCNGGAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 OY 368 TCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 427
 DB 241 WSNCCNGATTTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 OY 428 GTTCT 487
 DB 301 GTTCT 360
 OY 488 GCTGACGACCGGCTGCGCCCATTTATGATGATGATGATGATGATGATGATGATGAT 547
 DB 361 GCGNGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 OY 548 GCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
 DB 421 GCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 OY 608 GAGGACCTGTTGAGTGAAGCTGCTGACAGAGGACCTGTTGAGTGAAGCTGCTGCTCA 667
 DB 481 GARGCNCNGTNGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540

OY 668 GAGGACCTGTTGAGTGAAGCTGCTGACAGAGGACCTGTTGAGTGAAGCTGCTGCTCA 727
 DB 541 GARGCNCNGTNGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 OY 728 GCGACCTGCTGCGCCGAGAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 784
 DB 601 GCGACCTGCTGCGCCGAGAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 657

RESULT 10

AAS20592 ID AAS20592 standard; cDNA; 657 BP.

XX AAS20592;

XX 23-APR-2002 (first entry)

XX Human zsig63 degenerate cDNA coding sequence.

XX Human; zsig63; chromosome 4q12-q13; salivary protein; antimicrobial; ss;
 KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
 KW gastrointestinal disease; urinary tract infection; vaginal infection;
 KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
 KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
 KW chronic bronchitis; gene therapy; protein therapy; gene.

XX Homo sapiens.

XX US6331413-B1.

XX 18-DEC-2001.

XX 17-MAR-2000; 2000US-0527345.

XX 17-MAR-1999; 99US-124820P.

XX (ZYMO) ZYMOGENETICS INC.

XX Adler DA, Sheppard PO;

XX WPI; 2002-096707/13.

XX Polynucleotides encoding salivary proteins useful as anti-microbial
 agents -

XX Claim 3; Column 51-52; 29pp; English.

XX The invention relates to a polynucleotide derived from the 4q12-q13
 CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
 CC secreted salivary protein with anti-microbial activity. Due to their
 CC microbial activity, the sequences can be used in the study of microbial
 CC infections, e.g. for recombinant production of anti-microbial proteins.
 CC The sequences can be used in the treatment of tooth decay, periodontal
 CC disease, thrush, gastrointestinal disease, urinary tract infections,
 CC vaginal infections, skin infections, epithelial wounds, chronic tissue
 CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
 CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
 CC represents a degenerate cDNA encoding human zsig63.

XX Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;

Query Match 45.6%; Score 460; DB 24; Length 657;
 Best Local Similarity 61.0%; Pred. No. 2.2e-89;
 Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0;

OY 128 ATGAAGCTTCCTCTGGGCGCTGATGATGTTGCTTTGGCAAGAGAGCGGTTTC 187
 DB 1 ATGAARNTNTNTTGTGGCMTGATGHTGTGTGTCGTCMGAARAGNNAGNTTY 60
 OY 188 CCTTCATTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
 DB 61 CCTTTATHTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

[illegible]

RESULT 11	
ABX93595	
ID	ABX93595 standard, DNA, 657 BP.
XX	
AC	ABX93595,
XX	
DT	28-MAY-2003 (first entry)
XX	
DE	Human zsig63 degenerate sequence.
XX	
KW	ds; zsig63; adhesin; salivary gland; dental carries;
KW	periodontal disease; thrush; gastrointestinal disease; epithelial wound;
KW	urinary tract infection; vaginal infection; skin infection;
KW	pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
KW	lung infection; cystic fibrosis; lung dysfunction; digestive;
KW	salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
KW	chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW	cell culture media; gene therapy; human chromosome 4q12-4q13;
XX	dentinogenesis imperfecta; dentin dysplasia type II.
OS	Synthetic.
XX	
US	US2002173027-A1.
XX	
PD	21-NOV-2002.
XX	
PF	03-AUG-2001; 2001US-0922469.
XX	
PR	17-MAR-1999; 99US-124820P.
PR	17-MAR-2000; 2000US-0527345.
XX	
PA	(ADLER/) ADLER D A.
PA	(SHEP/) SHEPPARD P O.
XX	
FI	Adler DA, Sheppard PO,
XX	

XX	WPI; 2003-328428/31.
PT	Novel isolated zsig63 polypeptide, member of the adhesion family, useful
PT	for treating dental caries, periodontal disease, thrush,
PT	gastrointestinal disease, urinary tract infections, vaginal infections,
PT	skin infections
PS	-
PS	Claim 4; Page 28; 32pp; English.
XX	The invention relates to an isolated zsig63 polypeptide comprising at
CC	least 90% identity to an amino acid sequence which comprises domain 1 of
CC	zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
CC	included are the polynucleotide encoding zsig63, a zsig63 expression
CC	vector, a cultured cell comprising the vector and expressing the protein,
CC	a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37,
CC	38-126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC	zsig63 reporter gene construct to identify zsig63 agonists, and
CC	producing an anti-zsig63 antibody using zsig63 immunogenic peptides,
CC	zsig63 is useful for detecting in a test sample, the presence of
CC	antagonist of zsig63 protein activity. Zsig63 has antimicrobial
CC	activity and since exhibits high expression in salivary gland, can be
CC	used for treating dental caries, periodontal disease, thrush, and
CC	gastrointestinal disease, urinary tract infections, vaginal infections,
CC	skin infections and other epithelial wounds. The polypeptides can be
CC	used to establish normal microflora and protect against pathogenic
CC	colonization and invasion. Zsig63 can also be used for providing
CC	pro-inflammatory activity for treating chronic, tissue damage
CC	particularly in areas having limited or damaged vascular system, e.g.
CC	in diabetes, and for treating immunocompromised AIDS patients or in
CC	individuals that have undergone chemotherapy, radiation treatment, for
CC	treating lung infections e.g. in cystic fibrosis. Detection of zsig63
CC	polypeptide at relatively high levels in the trachea may indicate that
CC	such polypeptides may serve as a marker of lung dysfunction. Zsig63 is
CC	also useful in diagnosing conditions associated with salivary gland or
CC	lung dysfunction including salivary gland carcinoma, Pneumocystis carini
CC	infection, emphysema, chronic bronchitis, prostate dysfunctions such
CC	as prostate adenocarcinoma, aiding digestion, and as components of
CC	defined cell culture media and may be used to replace serum that is
CC	commonly used in culture. The DNA is useful in gene therapy applications
CC	to increase or inhibit zsig63 activity, and for detecting abnormalities
CC	on human chromosome 4 (e.g. 4q12-q4l3), associated with dentinogenesis
CC	imperfecta, and dentin dysplasia type II). Zsig63 is an adhesion family
CC	member. The present sequence represents all possible sequences that
CC	may encode zsig63.
CC	
SQ	Sequence 657 BP; 72 A; 150 C; 114 G; 65 T; 256 other;
	Query Match 45.6%; Score 460; DB 25; Length 657;
	Best Local Similarity 61.0%; Pred. No. 2.2e-89;
	Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0
OY	128 ATGAAGCTTCCTCCGTTGGGCGCTGCATGTATAGTGTGGCTTTTGCAAGAGACGCGTTC 187
Ddb	1 ATGAARITNTNTNTNTGCGCCTGTGATHGTNTGTCNGCNTTTCGCMGNAABRMGNMNTTY 60
OY	188 CCCTTCATTGGTGAGATGACAAATGACGATSGTACCACCATTCATTCCTGTGAATATT 247
Ddb	61 CCNTTATAGHNGARGAAGAAYAAVGAAYGANGCAVCNNTYNCAICCMNSNYTNAAVATH 120
OY	248 CCTTATGGCATACGGAATTTACCATCTCTCTTTATTAATGCGCCAGTGAATACATGCC 307
Ddb	121 CCNTAATGAGNATHMGNAAYTNCCNCNCNCNTNTAATYATVMGNCNGTNAAYCNGTNCN 180
OY	308 AGTTACCTGGGAADACTTACACGACACAGAGGTACCTGATACCCGATCTACT 367
Ddb	181 MSNTRATCCGNNAAIYACNTATAACGATAACNGANTTNCCMSSTATACCTGATHTTNACN 240
OY	368 TCTCCTGGATTCCCCTATGCTTATCACATCCGTGTGTTTTCCCTTAGTACTAGTTGAT 427
Ddb	241 MSNCGNGNTTYCCNTATGATNTATCAVATTHGNGSNTTTYCCNYTMGNAACNARBATMAAY 300
OY	428 GTTCTCTCTCCCTCCTAGAGGGTTTCCCGTTTGTCCCTCCTTCAAGTTTTCACAGA 487

301 AGTCCCCAGTTACCCCTGGGATACTTACACTGACACAGGGTACCTTCGATCCCTGGAT 30

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Db      301 AGTCCCAAGTACCCCTGGGAATAACTTACACTGACACAGAGGGTTACCTTCGATCCCTGGAT 360
Oy      361 TCTAACTTCTCCTGGATTCCCTTAATGTATATCAATCCGGTGTTCCTTACCTACTCA 420
Db      361 TCTAACTTCTCCTGGATTCCCTTAATGTATATCAATCCGGTGTTCCTTACCTACTCA 420
Oy      421 GTTGAATGTTCCCTCTCCCTCTCTAGGGGTTTCCGGTTGTCCCTCTCAAGGTTTTT 480
Db      421 GTTGAATGTTCCCTCTCTCCCTCTCTAGGGGTTTCCGGTTGTCCCTCTCAAGGTTTTT 480
Oy      481 TTCAAGCAGCTGACGACCCCGCTGCCACCCTATATTGACGTAGCCTGTGACCTGACCC 540
Db      481 TTCAGCAGCTGACGACCCCGCTGCCACCCTATATTGACGTAGCCTGTGACCTGACCC 540
Oy      541 TCTTACAGCACAACCTGTATGACAGCTAGGCTGTGTGACAGGGGCCCTGTGGACCTAGCC 600
Db      541 TCTTACAGCACAACCTGTATGACAGCTAGGCTGTGTGACAGGGGCCCTGTGTGACCTAGCC 600
Oy      601 TGCTGACAGGACCACTGTGTGAGCTAGGCTGTGTGACAGAGGCACTGTGACCTGAGCC 660
Db      601 TGCTGACAGGACCACTGTGTGAGCTAGGCTGTGTGACAGAGGCACTGTGTGACCTAGCC 660
Oy      661 TGCTGACAGGACCACTGTGTGAGCTAGGCTGTGTGACAGAGGCACTGTGTGACCTAGCC 720
Db      661 TGCTGACAGGACCACTGTGTGAGCTAGGCTGTGTGACAGAGGCACTGTGTGACCTAGCC 720
Oy      721 TGCTTACAGGCAAGCCCTGTGAGCCCAACACCTGACCCCTCCCTCTTGAACAAGGAAA 780
Db      721 TGCTTACAGGCAAGCCCTGTGAGCCCAACACCTGACCCCTCCCTCTTGAACAAGGAAA 780
Oy      781 TCAGTGAATTTCTGTAGAGAGTACAGTGGGTTCAATTTCTATCTAGTGCAGAAATAGT 840
Db      781 TCAGTGAATTTCTGTAGAGAGTACAGTGGGTTCAATTTCTATCTAGTGCAGAAATAGT 840
Oy      841 GAAATCTCAAAAGTTTTCTTTTCCAAAGACTATTTCAATTCGTGTGTATTCAGAGT 900
Db      841 GAAATCTCAAAAGTTTTCTTTTCCAAAGACTATTTCAATTCGTGTGTATTCAGAGT 900
Oy      901 ATTCAATCTCAATCATATGATTTGTGTGGTAGTTTTTCCCTGACCTTAATTAATTTGA 960
Db      901 ATTCAATCTCAATCATATGATTTGTGTGGTAGTTTTTCCCTGACCTTAATTAATTTGA 960
Oy      961 AAAAAATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008
Db      961 AAAAAATTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008

RESULT 2
; Sequence 3, Application US/09527345
; Patent No. 6311413
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/527,345
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide sequence for zsig63
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C or G
; US-09-527-345-3

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Query Match 45.6%; Score 460; DB 4; Length 657;
Best Local Similarity 61.0%; Pred. No. 5,6e-102;
Matches 401; Conservative 103; Mismatches 153; Indels 0; Gaps 0.

QY 128 ATGAAGCTTCCTCTTGGGGCTCGATGTGATGTGTGCTTTTGCAAGAAAGACGGTTC 187
DB 1 ATGAARYYTNNTYNTGGGCGNTGATGHTGTGTGNGTNGTTCGCMGMAAAMGMMGNTTY 60
QY 188 CCTTCATTTGTGAGGAATGACAATGAGAGATGGTACACCCACTCACTCATCTCTGTAATTT 247
DB 61 CCNTTAAHGGNGAGAGAAAGATPAAAGAGAYAGANCAACNTYNCAICCMWSYTNAAAYATH 120
QY 248 CCTTATGGCATACGGAAATTTTACCACTCTCTTTATTTATTCGCCAGTGAATACAGTCCCC 307
DB 121 CCNTAATYAGNATHMGMAAYTTTCCNCCNCCNCAVNTNTAATATATYATMCCNGTMAAAYACNGTNCN 180
QY 308 AGTTAACCTTGGGAATATCTTAACACTGACACAGAGGTTACTTGTAATCCCTGGATTTCTACT 367
DB 181 WSNATYCCNGNNAAYACNTAAYACNGAAYACNGAGNTYCCNMSNTAYCCNTGATHTYTNACN 240
QY 368 TCTCTGGAATTCCTCATGTCTAACATCCGTGTTTCCCTTAAGTACTCAGTGTGAT 427
DB 241 WSNCCNGGNTTYCCNTAATGINTAYCAVATHMGNGNTTYCCNYTNGCAACARCTNAAAY 300
QY 428 GTTCCTCTCTCCCTCTTACGAGGGGTTTCCGTTTGTCCCTCTCAAGTTTATTTTTCACAGA 487
DB 301 GTNCCNCCNYTNCNCCCMGNGGNTTYCCNTTGTGTCNCCNCCMSMGNTTYYTWSNCCN 360
QY 488 GCTGACAGACCCGCTGCCCCCACTAATGACAGCTGAGCTGTGACGTGACCTCTTTACA 547
DB 361 GCGNGGNCNCNCGNCGNCCNCAATHTGNCNGNARCCNGGNGCNGCNCNCTYTNACN 420
QY 548 GCCACACCTGTGACAGCTGAGCTGTGTCAGAGGGCCCTGTGTTGACGTGAGACCTGTGCA 607
DB 421 GCNACNCCNGTNGCNGCNGARCCNGCNGCNGNCCNGTNGCNGCNGARCCNGCNGCN 480
QY 608 GAGGACCTGTGAGCTGAGCTGTGCTCAGAGGACACTGTTGACGTGAGCTGTGCTCA 667
DB 481 GARGCNCNCGTNGAGCNGARCCNGCNGCNGARCGCNCNGTNGCNGCNGARCCNGCNGCN 540
QY 668 GAGGACCTGTGAGTGAAGCAGCTGACAGAGGAACCTTCAACAGCTGAGCTGTGCTACA 727
DB 541 GARGCNCNCGTNGAGTGTGARCCNGCNGCNGARCCNMSNCCNGCNGARCCNGCNGCN 600
QY 728 GCCAAGCTGTGCTGCCCAAGAACTTCACTTCTCTCTTGTGAACAGGCAATATAG 784
DB 601 GCNARCCNCGNCGCNGARCCNCAVCCNMSNCCNMTYNGARCCAGCNAAYCAR 657

RESULT 3
US-08-728-323A-1/c
Sequence 1, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James U.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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Query Match	12.0%;	Score 121.2;	DB 2;	Length 3489;
Best Local Similarity	58.7%;	Pred. No. 8.9e-20;		
Matches 210; Conservative	0;	Mismatches 148;	Indels 0;	Gaps 0;

[illegible]

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/ RESULT 4
/ US-09-298-568-1/C
/ Sequence 1, Application US/09298568
/ Patent No. 6322792
/ GENERAL INFORMATION:
/ APPLICANT: Kieff, Elliott D.
/ APPLICANT: Ballestas, Mary E.
/ APPLICANT: Kaye, Kenneth M.
/ TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
/ TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
/ FILE REFERENCE: 16412-10001R
/ CURRENT APPLICATION NUMBER: US/09/298, 568
/ CURRENT FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 60/109, 422
/ EARLIER FILING DATE: 1998-11-19
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3489
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; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

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Query Match	12.0%	Score 121.2	DB 4	length 3489
Best Local Similarity	58.7%	Pred. No. 8.9e-20		
Matches 210; Conservative	0	Mismatches 148	Indels 0	Gaps 0

Qy	413	GCTACGATGAAATGTCCTCCCTCCCTCCCTCCTAGAGGGATTCGCGTTGACCCCTTCA	472
Db	2188	GCTGCTATCCTGCTGCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCAT	2129
Qy	473	AGGTTTTTTCAGCAGCTGAGAGCACCCGCTGCCCACTTAATGACGCTGAGCCTGTGCA	532
Db	2128	CCTGCTGCTCCTGCTCATCCTGCTGCTCCTGCTCATCCTGCTGCTCATCCTGCTGCT	2065
Qy	533	GCTGCACTCTTACAGCCACACCTGTAGACGCTGCTGTCGAGGGGCCCTGTGTGCA	592
Db	2068	GCTCATCCTGCTGCTGCTCATCCTGCTGCTCATCCTGCTGCTCATCCTGCTGCT	2009
Qy	593	GCTGAGCCTGCTGCAGAGGACCTGTTGAGCTGAGCCTGCTGCAGAGGACCTGTTGCA	652
Db	2008	GCTCATCCTGCTGCTGCTCATCCTGCTGCTCATCCTGCTGCTCATCCTGCTGCT	1949
Qy	653	GCTGAGCCTGTCAGAGGACCTGTTGAGCTGAGCGACGCTGTCAGAGGAACTTACCA	712
Db	1948	GCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTCATCCTGCTGCT	1889
Qy	713	GCTGAGCCTGTCAGAGGACCGTCGCCCCAGAACCTTCACTTCCCTCTTGG	770
Db	1888	GCTATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTG	1831

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RESULT 5
US-09-410-399-1/c
; Sequence 1, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Cotter, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; TITLE OF INVENTION: to Genomic Host DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

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Query Match	12.0%	Score 121.2	DB 4	Length 3489
Best Local Similarity	58.7%	Pred. No. 8.9e-20		
Matches 210	Conservative 0	Mismatches 148	Indels 0	Gaps 0
Qy	413	GCTACTCAGTTGAATGTTCTCTCTCTCCCTCTTACGGGGTTTCCGTTTGTCCCTCTTCA	472	
Db	2188	GCTGCTCATCTGCTGCTGCTGCTCATCTCTGCTCTGCTCATCTCGCTGCTCTGCTCAT	2129	
Qy	473	AGGTTTTTTTCAGCAGCGCAGCACCAGCGGCCACCTATTTCAGCTGACCTGCTGCA	532	
Db	2128	CTGCTGCTCTGCTCATCTGCTGCTCTCTCTATCTGCTGCTGCTCATCTGCTGCT	2065	
Qy	533	GCTGCACCTCTTACAGCCACACCTGTACGACCTGAGCTGCTGACGAGGAGCCCTGTTCGA	592	
Db	2068	GCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCT	2009	
Qy	593	GCTGAGCTGCTGACGAGGACACCTGTGAGCTGAGCTGCTGACGAGGACACCTGTTTGA	652	
Db	2008	GCTATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCT	1949	

QY 653 GGTGAGCCTGCTGAGAGGACCTGTTGAGTGGAGCCAGCTGAGAGGAACTTTCACCA 712
DB 1948 GCTATCTGCTGCTGCTGCTATCTGCTGCTGCTATCTGCTGCTGCTGCTGCTGCT 1889
QY 713 GCTGAGCCTGCTGACGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
DB 1888 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1891

RESULT 6
US-08-770-379-20

; Sequence 20, Application US/08770379
; Patent No. 549564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-20

Query Match 12.0%; Score 121.2; DB 2; Length 32207;
Best Local Similarity 58.7%; Pred. No. 2.6e-19;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 413 GCTACTCAGTTGAATGTTCA 472
DB 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCAT 19868
QY 473 AGGTTTTTTCAGAGCTGAGAGACCCGCTGCCCACTATTGAGCTGAGCTGCTGCA 532
DB 19869 CCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19928
QY 533 GCTGACCTCTTACAGGACCACTGTAGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 592
DB 19929 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19988
QY 593 GCTGAGCCTGCTGAGAGGACCTGTTGAGCTGAGCTGAGCTGCTGAGAGGACCTGTTGCA 652
DB 19989 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20048

QY 653 GGTGAGCCTGCTGAGAGGACCTGTTGAGTGGAGGACCTGAGAGGAACTTTCACCA 712
DB 20049 GCTATCTGCTGCTGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20108
QY 713 GCTGAGCCTGCTGACGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
DB 20109 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20166

RESULT 7
US-08-757-669A-20

; Sequence 20, Application US/08757669A
; Patent No. 618751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-669A-20

Query Match 12.0%; Score 121.2; DB 3; Length 32207;
Best Local Similarity 58.7%; Pred. No. 2.6e-19;
Matches 210; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
QY 413 GCTACTCAGTTGAATGTTCA 472
DB 19809 GCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCAT 19868
QY 473 AGGTTTTTTCAGAGCTGAGAGACCCGCTGCCCACTATTGAGCTGAGCTGCTGCA 532
DB 19869 CCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19928
QY 533 GCTGACCTCTTACAGGACCACTGTAGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 592
DB 19929 GCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19988
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Dd	GCTCATCCTGCTGCTGCTCATCCGCTGCTCATCTGCTGCTCATCTGCTGCT	20048
Db	19989	
Qy	GCTGAGCCTGCTGTGAGAGCAACCTGTGAGATGAGAGCAAGCTCAGAGAACCTTCACCA	712
Qy	653	
Dd	20049	
Qy	GCTATCTCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCT	20108
Dd	713	
Qy	GCTGAGCCTGCTACGAGCAACCTGCTGCTGCCCAAGAACCTTCCTCTCTCTTG	770
Dd	20109	
Qy	GCTATCTCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTG	20166

RESULT 8
US-09-230-371A-20
: Sequence 20, Application US/09230371A

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: PATENT NO: 6348586
: GENERAL INFORMATION:
: APPLICANT: Chang, Yuan
: APPLICANT: Bohenzky, Roy A
: APPLICANT: Russo, James J
: APPLICANT: Edelman, Isidore S
: APPLICANT: Moore, Patrick S
: TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
: FILE REFERENCE: 45185-G-PCT-US
: CURRENT APPLICATION NUMBER: US/09/230,371A
: CURRENT FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: PCT/US97/13346
: PRIOR FILING DATE: 1997-07-22
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 32207
: TYPE: DNA
: ORGAINISM: Kaposi's sarcoma-associated herpesvirus
: US-09-230-371A-20

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Query Match	12.0%;	Score 121.2;	DB 4;	Length 32207;
Best Local Similarity	58.7%;	Pred. No. 2.6e-19;		
Matches 210; Conservative	0;	Mismatches 148;	Indels 0;	Gaps 0;

Oy	413	GCTACTAGTTGATGATGTTCCCTCCCTCCCTCCCTAAGGGATTTCCCGTTTGGCCCTCTTGA	472
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Db	19869	CTCTGCTGCTCTGCTCATCTGCTGCTCTGCTCATCTGCTGCTCATCTGCTGCTCATCTGCTGCT	19928
Oy	533	GCTGCACCTCTTACAGCACCACTGTTAGACAGTGAAGCCTCTGACAGGGGCCCTGTTTGA	592
Db	19929	GCTCATCTGCTGCTGCTGCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTCATCTGCTGCT	19988
Oy	593	GCTGAGCCTGCTGCAGAGGACCTGTTGAGCTGAGCCTGCTGCAGAGGACCTGTTTGA	652
Db	19989	GCTCATCTGCTGCTGCTGCATCTGCTGCTGCTCATCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCT	20048
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RESULT 9
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; Sequence 3, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Rannum, Laura P. W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION

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: FILE REFERENCE: 11000900101
: CURRENT APPLICATION NUMBER: US/09/161,585
: CURRENT FILING DATE: 1998-10-28
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 1037
: TYPE: DNA
: ORGANISM: Artificial Sequence
FEATURES:
: OTHER INFORMATION: Description of Artificial Sequence: cdva
: OTHER INFORMATION: comprising exons E, C, and A
US-09-161-585-3

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Query Match	9.9%	Score 100;	DB 4;	Length 1037;
Best Local Similarity	56.8%	Pred. No. 6.6e-15;		
Matches 184; Conservative	0;	Mismatches 140;	Indels 0;	Gaps 0;

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RESULT 10
US-09-181-585-1
; Sequence 1, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Rannum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 11000900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-181-585-1

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	Best Local Similarity	5.8%;	Pred. No. 76-15;		
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Db	403	TTCTTGCGTAGACCCTGGGCTCTTCACGTGAAACCTGGCTTTACTACTACTAC	462		
OY	466	TCCTTCAGGTTTTTTTCAGCAGCTGCAGCACCCGCTGCCCACTTATTCAGCTGAC	525		
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Wed Jan 21 09:54:18 2004

us-09-923-236-1.mf

Page 8

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Job time : 92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	1008	9	US-09-922-480-1
2	1008	100.0	1008	9	US-09-923-236-1
3	1008	100.0	1008	10	US-09-922-469-1
4	981.6	97.4	1325	11	US-09-746-783-105
5	896.4	88.9	959	13	US-10-231-417-41
6	460	45.6	657	9	US-09-922-480-3
7	460	45.6	657	9	US-09-923-236-3
8	460	45.6	657	10	US-09-922-469-3
9	121.2	12.0	3489	13	US-10-294-804-1
10	100	9.9	1037	12	US-10-373-667-3
11	100	9.9	1159	12	US-10-373-667-1
12	100	9.9	1471	12	US-10-373-667-2
13	98.2	9.7	2108	10	US-09-962-832-225
14	92.4	9.2	1101	9	US-09-874-062-2
15	89.2	8.8	2183	12	US-10-104-047-1064

C 16	87.6	8.7	1101	9	US-09-874-062-2	Sequence 2, Appl1
C 17	85.2	8.5	1926	13	US-10-294-804-3	Sequence 3, Appl1
C 18	85.2	8.5	8705	15	US-10-291-230-14	Sequence 14, Appl1
C 19	85.2	8.5	8705	15	US-10-291-249-14	Sequence 14, Appl1
C 20	85.2	8.5	9600	13	US-10-278-751-1	Sequence 1, Appl1
C 21	85.2	8.5	10233	13	US-10-050-898-283	Sequence 283, App
C 22	85.2	8.5	10285	13	US-10-050-902-283	Sequence 283, App
C 23	84	8.3	1037	12	US-10-373-667-3	Sequence 3, Appl1
C 24	84	8.3	1159	12	US-10-373-667-1	Sequence 1, Appl1
C 25	84	8.3	1471	12	US-10-373-667-2	Sequence 1, Appl1
C 26	83.6	8.3	477	13	US-10-357-322-1	Sequence 1, Appl1
C 27	83	8.2	2183	12	US-10-104-047-1064	Sequence 1064, Ap
C 28	78.2	7.8	16442	12	US-10-374-077-208	Sequence 208, App
C 29	77.8	7.7	422	10	US-09-738-973-337	Sequence 337, App
C 30	77.8	7.7	422	10	US-09-854-133-337	Sequence 337, App
C 31	77.8	7.7	422	15	US-10-144-649A-337	Sequence 337, App
C 32	75	7.4	14859	12	US-10-051-874-55	Sequence 55, Appl
C 33	73.4	7.3	9369	13	US-10-200-562-190	Sequence 190, App
C 34	73.4	7.3	9369	13	US-10-237-551-190	Sequence 190, App
C 35	73.4	7.3	9369	13	US-10-237-551-247	Sequence 247, App
C 36	73.4	7.3	154746	13	US-09-827-688-8	Sequence 8, Appl1
C 37	73.2	7.3	14859	12	US-10-051-874-55	Sequence 55, Appl
C 38	72.6	7.2	1388	12	US-10-264-049-518	Sequence 518, App
C 39	72.2	7.2	469	13	US-10-029-386-20613	Sequence 20613, A
C 40	72.2	7.2	5379	15	US-10-128-714-5305	Sequence 5305, Ap
C 41	71.8	7.1	2404	12	US-10-104-047-1740	Sequence 1740, Ap
C 42	71.8	7.1	3439	12	US-10-161-927-53	Sequence 53, Appl
C 43	71.6	7.1	628	13	US-10-029-386-22859	Sequence 22859, A
C 44	71.6	7.1	1008	9	US-09-922-480-1	Sequence 1, Appl1
C 45	71.6	7.1	1008	9	US-09-923-236-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-922-480-1
Sequence 1, Application US/09922480
Patent No. US20020081701A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SECRETED SALIVARY ZS163 POLYPEPTIDE
FILE REFERENCE: 97-71
CURRENT APPLICATION NUMBER: US/09/922,480
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/124,820
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1008
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (128)...(784)
US-09-922-480-1
Query Match 100.0%; Score 1008; DB 9; Length 1008;
Best Local Similarity: 100.0%; Pred. No. 1; ie-236;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACAGACTAAAAGCCATGATCTTCTCTCTAAAGAGAAAATTAATTT 60
1 AGACAGACTAAAAGCCATGATCTTCTCTCTAAAGAGAAAATTAATTT 60
DB 61 TAAATATCATGGCTATTTCTTAAACAAATTAATTAATGTTAATATCATAGGCTC 120
61 TAAATATCATGGCTATTTCTTAAACAAATTAATTAATGTTAATATCATAGGCTC 120
QY 121 AATCAATGAAGCTTCCTCTGGGCTGATGATGTTGCTTTTGCAGAGAG 180
121 AATCAATGAAGCTTCCTCTGGGCTGATGATGTTGCTTTTGCAGAGAG 180

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Db      121 AATCAAAATGAAGCTTCTCTTGGGCTGACATGTGATGTGCTTTTGAAGAAGAG 180
Qy      181 AGGTTTCCCTTCATTTGGTGAAGATGACAAATGATGTGACCCACTTCATCCATCTT 240
Db      181 AGGTTTCCCTTCATTTGGTGAAGATGACAAATGATGTGACCCACTTCATCCATCTT 240
Qy      241 GAATATTCCTTATGAGATGAGAAATTTACCACTCTCTTTATTAAGCCAGTAATAC 300
Db      241 GAATATTCCTTATGAGATGAGAAATTTACCACTCTCTTTATTAAGCCAGTAATAC 300
Qy      301 AGTCCCAAGTACCTTGGGAATACTTACATGACACAGGGTTACCTTGTATCCCTGAT 360
Db      301 AGTCCCAAGTACCTTGGGAATACTTACATGACACAGGGTTACCTTGTATCCCTGAT 360
Qy      361 TCTAATCTTCTGGAATTCCTTATGTCTATCAATCCGTGTTTCCCTTATGCTACTCA 420
Db      361 TCTAATCTTCTGGAATTCCTTATGTCTATCAATCCGTGTTTCCCTTATGCTACTCA 420
Qy      421 GTTGAATGTTCTCTCTCTCTCTCTAGGGGTTTCCGTTTGTCCCTCTTCAAGGTTTT 480
Db      421 GTTGAATGTTCTCTCTCTCTCTCTAGGGGTTTCCGTTTGTCCCTCTTCAAGGTTTT 480
Qy      481 TTCAAGAGCTGACAGCCCGCTGACCCCACTATTGACAGCTGCTGACAGCTGAC 540
Db      481 TTCAAGAGCTGACAGCCCGCTGACCCCACTATTGACAGCTGCTGACAGCTGAC 540
Qy      541 TCTTACAGCACAACCTGTAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 600
Db      541 TCTTACAGCACAACCTGTAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 600
Qy      601 TCTCTAGAGGACACCTGTGAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 660
Db      601 TCTCTAGAGGACACCTGTGAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 660
Qy      661 TCTCTAGAGGACACCTGTGAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 720
Db      661 TCTCTAGAGGACACCTGTGAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 720
Qy      721 TGTCTAGAGGACACCTGTGAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 780
Db      721 TGTCTAGAGGACACCTGTGAGAGCTGAGCTGTGCAAGGGGCTCTGTGTGACAGCTGAG 780
Qy      781 TCAAGGAATTCCTAGAGAGTACATGGTTCTATTCTATGATGATGACAAATTAAGT 840
Db      781 TCAAGGAATTCCTAGAGAGTACATGGTTCTATTCTATGATGATGACAAATTAAGT 840
Qy      841 GAAATCTACAAAGTTTCTTTCTTTCCAAAGACTATTTCATCTGTGTATTCAGAGT 900
Db      841 GAAATCTACAAAGTTTCTTTCTTTCCAAAGACTATTTCATCTGTGTATTCAGAGT 900
Qy      901 ATTCAATCTACATCATTTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA 960
Db      901 ATTCAATCTACATCATTTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA 960
Qy      961 AAAAATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008
Db      961 AAAAATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1008

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RESULT 2
US-09-923-236-1

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; Sequence 1, Application US/09923236
; Patent No. US2002090677A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9

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; SOFTWARE: FastSPQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)...(784)
US-09-923-236-1

Query Match      100.0%; Score 1008; DB 9; Length 1008;
Beet Local Similarity 100.0%; Pred. No. 1.e-236;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 AGACGACTAATAAAGCCATATTTCTTCTCTCTCTTAAAGAAAGAAATTAATT 60
Qy      61 TAAATATCATTTGGGATTTTCTAATAACATTAATTAATAGTTAAATTAATTATAGGGTC 120
Db      61 TAAATATCATTTGGGATTTTCTAATAACATTAATTAATAGTTAAATTAATTATAGGGTC 120
Qy      121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATGTATGTGTCTTTTGAAGAAAG 180
Db      121 AATCAAAATGAAGCTTCTCTTGGGCTGCAATGTATGTGTCTTTTGAAGAAAG 180
Qy      181 AGGTTTCCCTTCATTTGGTGAAGATGACAAATGATGTGTGACCCACTTCATCTCT 240
Db      181 AGGTTTCCCTTCATTTGGTGAAGATGACAAATGATGTGTGACCCACTTCATCTCT 240
Qy      241 GAATATTCCTTATGAGATGAGAAATTTACCACTCTCTTATTAATGAGCCAGTAATAC 300
Db      241 GAATATTCCTTATGAGATGAGAAATTTACCACTCTCTTATTAATGAGCCAGTAATAC 300
Qy      301 AGTCCCAAGTACCTTGGGAATACTTACATGACACAGGGTTACCTTGTATCCCTGAT 360
Db      301 AGTCCCAAGTACCTTGGGAATACTTACATGACACAGGGTTACCTTGTATCCCTGAT 360
Qy      361 TCTAATCTTCTGGAATTCCTTATGTCTATCAATCCGTGTTTCCCTTATGCTACTCA 420
Db      361 TCTAATCTTCTGGAATTCCTTATGTCTATCAATCCGTGTTTCCCTTATGCTACTCA 420
Qy      421 GTTGAATGTTCTCTCTCTCTCTCTAGGGGTTTCCGTTTGTCCCTCTTCAAGGTTTT 480
Db      421 GTTGAATGTTCTCTCTCTCTCTCTAGGGGTTTCCGTTTGTCCCTCTTCAAGGTTTT 480
Qy      481 TCAAGGAATTCCTAGAGAGTACATGGTTCTATTCTATGATGATGACAAATTAAGT 840
Db      481 TCAAGGAATTCCTAGAGAGTACATGGTTCTATTCTATGATGATGACAAATTAAGT 840
Qy      841 GAAATCTACAAAGTTTCTTTCTTTCCAAAGACTATTTCATCTGTGTATTCAGAGT 900
Db      841 GAAATCTACAAAGTTTCTTTCTTTCCAAAGACTATTTCATCTGTGTATTCAGAGT 900

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OY	250	TTATGGCATAAGSAATTTTACCACTCTCTTTATATGCGCCAGTAATATACAGTCCGAC	309
Db	249	TTATGGCATAAGSAATTTTACCACTCTCTTTATATGCGCCAGTAATATACAGTCCGAC	308
OY	310	TTACCTGGGAATACTTACACTGACACAGGGTTACCTTGTATCCCTGGATTCTAACCTC	369
Db	309	TTACCTGGGAATACTTACACTGACACAGGGTTACCTTGTATCCCTGGATTCTAACCTC	368
OY	370	TCCTGGATTCCCTTATGCTATCATCATCGTGGTATTTCCCTTAGCTACATGATGAATGT	429
Db	369	TCCTGGATTCCCTTATGCTATCATCATCGTGGTATTTCCCTTAGCTACATGATGAATGT	428
OY	430	TCCTCTCTCCCTCCTAGGGGTTTCCCGTTGTCCCTCCTTCAAGGTTTTTTTACAGAC	489
Db	429	TCCTCTCTCCCTCCTAGGGGTTTCCCGTTGTCCCTCCTTCAAGGTTTTTTTACAGAC	488
OY	490	TGCAGCACCCGCTGCCCCACCTATTGACGTAGCGCTGTGACGTGACGACCTTACACGC	549
Db	489	TGCAGCACCCGCTGCCCCACCTATTGACGTAGCGCTGTGACGTGACGACCTTACATC	548
OY	550	CACACCTGTAGACAGCTGAGCCTGTCTGACAGGGGCCCTGTGTGAGCTGAGCCTGTCTGACA	609
Db	549	CACACCTGTAGACATCTGAGCCTGTCTGACAGGGGCCCTGTGTGAGCTGAGCCTGTCTGACA	608
OY	610	GGCACCTGTGGAGAGCTGAGCCTGTCTGACAGGACCTGTGTGAGCTGAGCCTGTCTGACA	669
Db	609	GGCACCTGTGTGAGAGCTGAGCCTGTCTGACAGGACCTGTGTGAGCTGAGCCTGTCTGACA	668
OY	670	GGCACCTGTGTGAGAGTGAGCCAGCTGACAGAGGAACTTACACAGCTGAGCCTGTCTACGC	729
Db	669	GGCACCTGTGTGAGAGTGAGCCAGCTGACAGAGGAACTTACACAGCTGAGCCTGTCTACGC	728
OY	730	CAAGCTGTCTGCCCAAGAACTCACCCCTTCTCCCTCTTTGAACAGGCAAAATCAAGTAA	789
Db	729	CAAGCTGTCTGCCCAAGAACTCACCCCTTCTCCCTCTTTGAACAGGCAAAATCAAGTAA	788
OY	790	TTCTCTAAGAAGTACATGGGTTCAATTTCTATTCTGATGACAGAAATAGTAATATCAC	849
Db	789	TTCTCTAAGAAGTACATGGGTTCAATTTCTATTCTGATGACAGAAATAGTAATATCAC	848
OY	850	AAAAGTTTCTTCTTTTCCAAAGACATTTTCATTTCTGTTGATTTCAAGATTCATCTC	909
Db	849	AAAAGTTTCTTCTTTTCCAAAGACATTTTCATTTCTGATGATTCAGAGTATTCATCTC	908

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RESULT 5
US-10-231-417-41
; Sequence 41, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: P2019P1
; CURRENT APPLICATION NUMBER: US/10/231, 417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-417-41

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Query Match	88.9%;	Score 896.4;	DB 13;	Length 959;	
Best Local Similarity	98.8%;	Pred. No. 2.5e-209;			
Matches 923;	Conservative	1;	Mismatches 7;	Indels 3;	Gaps 2
QY	75	GGATTTTCTAAAAACAATAAATTTATAGGTCTAATATCTATAGGTCGAATCAAAATGAAGC	134		
DB	12	GGATTTTCTAAAAACAATAAATTTATAGGTCTAATATCTATAGGTCGAATCAAAATGAAGC	71		
QY	135	TTCTCCTTTGGGCGCGCATTTGATGTGTGCTTTTGCAGAGAAAGACGGTCCCTTCA	194		
DB	72	TTCTCCTTTGGGCGCGCATTTGATGTGTGCTTTTGCAGAGAAAGACGGTCCCTTCA	131		
QY	195	TTGTGAGAGATGACAAATGACATGCGTGCACCCACTTCATCTCGAATATTTCTTATG	254		
DB	132	TTGTGAGAGATGACAAATGACATGCGTGCACCCACTTCATCTCGAATATTTCTTATG	191		
QY	255	GCATACGGAAATTATACCACTCTCTTTATTTATGCGCCAGTAATACAGTCCCGAGTTAC	314		
DB	132	GCATACGGAAATTATACCACTCTCTTTATTTATGCGCCAGTAATACAGTCCCGAGTTAC	251		
QY	315	CTGGAAATPACTTACACTGACACAGGGTTACCTTGATCCCTGGATTTCTAACCTTCTCTG	374		
DB	252	CTGGAAATPACTTACACTGACACAGGGTTACCTTGATCCCTGGATTTCTAACCTTCTCTG	311		
QY	375	GATTCGCCCATGTCATATACATCCGGAGTTTTCCCTTACTCTACCTGAGTGAATGTTCTTC	434		
DB	312	GATTCGCCCATGTCATATACATCCGGAGTTTTCCCTTACTCTACCTGAGTGAATGTTCTTC	371		
QY	435	CTCTCCCTCTGAGGGGTTCCCGTTGTGCCCTCTTCAAGGTTTTTTTTCAGCAGCTGCAG	494		
DB	372	CTCTCCCTCTGAGGGGTTCCCGTTGTGCCCTCTTCAAGGTTTTTTTTCAGCAGCTGCAG	431		
QY	455	CACCCGCTGCCCACTCTATTTGACGCTGAGCCCTGCGACCTGCACCTCTTACGCCACAC	554		
DB	432	CACCCGCTGCCCACTCTATTTGACGCTGAGCCCTGCGACCTGCACCTCTTACGCCACAC	491		
QY	555	CTGTAGCAGCTAGGCTGCTGCAGGGGCCCTGTGTCAGACTGAGCTGTGCTGCTG--CAGAGGC	612		
DB	432	CTGTAGCAGCTAGGCTGCTGCAGGGGCCCTGTGTCAGACTGAGCTGTGCTGCTGCTG--CAGAGGC	551		
QY	613	ACCTGTTGAGC--TGAAGCTGCTGCAGAGGCACCTGTTGCAGAGCTGAGCCTGCTGCAGAGG	671		
DB	552	ACCTGTTGAGCCTTGAAGCTGCTGCTGCAGAGGCACCTGTTGCAGAGCTGAGCCTGCTGCAGAGG	611		

Qy	368	CTCTCGAATTCCTCCATATCTATCAACATCCGGATTTTCCCTAGACTACAGTGAAT	427
Db	241	MSNCCNGNTTTCNTATYGTNTAYCAATHHMGNGATTTTCNTTNGCMACNARYTAA	300
Qy	428	GTTCTCTCTCTCCCTCTAAGGGGGTTTCCCGTATTGTCCCTCTTCAAGATTTTTACGA	487
Db	301	GTNCCNCCNYTNCNCNNNGNGNTTTCNTTGTATNCNCNNMSNGMTTATTYWSNGCN	360
Qy	488	GCTGAGACACCCGCGCCACCTATTGCAAGTCACTGTGACCTGTGACACTCTTACA	547
Db	361	GCNGGNCNCNCNGCNGCNCNCNCNAATHGNCNGCNGCNGCNGCNGCNCNCNYTACN	420
Qy	548	GCACACCTGTAGACAGCTGAGCTGTGTGCAAGGGGGCCCTGTGTTCAGCTGAGCTGTGCA	607
Db	421	GCNACNCNCNTGNCNGCNGARCCNGCNGCNGCNGCNCNTGTGNCNGCNGARCCNGCNGCN	480
Qy	608	GAGGCACTGTGTGAGAGCTGAGCTGTGTGCAAGAGCACTGTGTTCAGCTGAGCTGTGCA	667
Db	481	GARGCNCNGTGTGNGCNGARCCNGCNGCNGAGARGCNCNGTGTGNCNGCNGARCCNGCNGCN	540
Qy	668	GAGGCACTGTGTGAGAGTGAAGCCAGCTGCAAGAGAACTTCAACAGTGAAGCTGTGACA	727
Db	541	GARGCNCNGTGTGNGTNGARCCNGCNGCNGAGARGCNCNWSNCCNCGCNGARCCNGCNGCN	600
Qy	728	GCGAAGCCGTGCGCCCAAGAACTCAACCTTTCCTCTCTTGAACAGGAAATTCAG	784
Db	601	GCNAARCCNCGCNCNCNARGCNCNAYCCNWSNCCNWSNTTNGARCAAGCNAATYCAR	657

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RESULT 8
US-09-922-469-3
; Sequence 3, Application US/09922469
; Patent No. US2002017027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS1G63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide sequence for zs1g63
; NAME/KEY: misc feature
; LOCATION: (1) ... (657)
; OTHER INFORMATION: n = A,T,C or G
US-09-922-469-3

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Query Match	45.6%	Score 460;	DB 10;	Length 657;
Best Local Similarity	61.0%	Pred. No. 1.9e-102;		
Matches 401;	Conservative 103;	Mismatches 153;	Indels 0;	Gaps 0

QY 128 TTGAAGCTTCTCCCTTGGGCGTCGATCTGATGTGTGGCTTTGACGAAGAACCGETTC 187
Db 1 ATGAARVYNYNYNYTNTGGCCTGTGAATGNTGTGTGTCGCTTGGCAGNNAARMCMGATY 60
QY 188 CCCTTCATTTGGTGAAGATACATGATGATGATGACCCCATTCATCATCTCTGAAATAT 247
Db 61 CCNTTATHTGGAGATGATGAATGAATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 248 CCTTATGCGATACGGAATTTACCACTCTCTTATTTATGCGCCAGTGAATACAGTCCCC 307
Db 121 CCNTATYGGNATHTGNNAAYATTCNCNCNCNTTATATATATATATATATATATATATATAT 180
QY 308 AGTTACCTTGGGAATATCTTACACTGACACAGGTTATCTTGGATATCCCTGGATTTCACT 367

Db 181 WSNATYCCNGGNAAYACHTAYACNGAYACNGENYTNCCMSWTATACNTGAGATHYTNACN 240

Qy 368 TCTCTGATYTCCTCCCTATGTCTATACATCCGTGGTTTTCCCTTAGCTACTGATGTAAT 427

Db 241 WSNCCNGENYTYCCNTAYGTNTAYCAVATHMNGENYTYCCNYTNGCNACNCARYTNAY 300

Qy 428 GTTCTCTCTTCCTCTCTAGGGGTTTTCCCGTTTTGTCCCTCTCTTCAAGGTTTTTTCAGA 487

Db 301 GTNCCNCCNYTNCNCNMNGENYTYCCNTTYGTNCCNCCMSNMGNITTTTTYTSNGCN 360

Qy 488 GGTGAGACACCGCTGGCCCACTTATGAGCTGAGCTGTGAGCTGACCTCTTACA 547

Db 361 GGNNGNCCNCCNGCNCNCNCNAITHGUNGNGARCCNGCNCNGCNCNCNTTNACN 420

Qy 548 GCCAACCTGTAGACAGCTGAGCTGTGCTCAGGGGCCCTGTTTGACGTGAGCCTGTGCA 607

Db 421 GCMNCNCNGTNGCNGCNGARCCNGCNCNGSNGCNCNGTNGCNGCNGARCCNGCNGCN 480

Qy 608 GAGGCACTGTGGAGCTGAGCCTGTGCTGAGAGGCACTGTTTGACGTGAGCCTGTGCA 667

Db 481 GARGCNCNGTNGCNGCNGARCCNGCNCNGARGCNCNGTNGCNGCNGARCCNGCNGCN 540

Qy 668 GAGGCACTGTTGGAGGTGAGCCTGAGGTCAGAGGAACTTACCAAGCTGAGGCTGTACA 727

Db 541 GARGCNCNGTNGAGTNGARCCNGCNCNGARGARCCNMSYCCNGCNGARCCNGCNGACN 600

Qy 728 GCCAAGCTGTGCTGCCAGAACTCAAGCCTTCTCCTCTCTTGAACAGGCAATATCG 784

Db 601 GCNAARCCNGCNCNGARCCNCAYYCCNMSNCCMSYTTGACARCCNAAYCAR 657

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RESULT 9
US-10-294-804-1/c
: Sequence 1, Application US/10294804
: Publication No. US20030133948A1
: GENERAL INFORMATION:
: APPLICANT: Robertson, Erle S.
: APPLICANT: Cotter, Murray A.
: TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
: TITLE OF INVENTION: to Genomic Host DNA
: FILE REFERENCE: UM-03778
: CURRENT APPLICATION NUMBER: US/10/294,804
: CURRENT FILING DATE: 2002-11-14
: PRIORITY APPLICATION NUMBER: US/09/410,399
: PRIOR FILING DATE: 1999-10-01
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3489
: TYPE: DNA
: ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-294-804-1

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Query Match	12.0%;	Score 121.2;	DB 13;	Length 3489;
Best Local Similarity	-58.7%;	Pred. No. 6.5e-19;		
Matches 210; Conservative	0;	Mismatches 148;	Indels 0;	Gaps 0;

QY	413	GCATACGATGGAAAGTTCCTCCCTCCCTCCCTAGGGGGTTTCCGGTTGTCCCTCTCA	472
Db	2188	GCTGCTCATCTGCTGCTGCTGCTCATCTGCTGCTCATCTGCTGCTCTCTCAT	212
QY	473	AGGTTTTTTTCAGCAGAGCTCAGACAACCCGCTCCCACTTATGCAAGTGAAGCTGCTCA	532
Db	2128	CTCTGCTGCTCTGCTGCATCTGCTGCTCTGCTCATCTGCTGCTGCATCTGCTGCT	2065
QY	533	GCTGCACCTTTTACAGCCACACCTGTAGACAGCTGAGCTGTCGACGGGGCCCTTTGCA	592
Db	2068	GCTCATCTCTGCTGCTGCATCTGCTGCTCTCATCTGCTGCTGCATCTGCTGCT	2005
QY	593	GCTAGAGCTGTCGACAGAGACACCTGTTGAACCTGAGCTGTCGACAGAGACACCTTTGCA	652
Db	2008	GCTCATCTGCTGCTGCATCTGCTGCTCTCATCTGCTGCTGCATCTGCTGCT	1944

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Search completed: January 16, 2004, 10:30:01
Job time : 397 secs

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OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 07:13:18 ; Search time 2130 Seconds
(without alignments)
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Title: US-09-923-236-1

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Perfect Score: 1008
Sequence:      1 agacagactaaaaagccat.....tagataatttagaccaatgg 1008

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :
ESI:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estrom:*
17: em_gse_hum:*
18: em_gse_inv:*
19: em_gse_pin:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_phg:*
27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Result No.	Score	Match	length	DB	ID	Description
1	703	69.7	703	2	HSMT075873	Bx485586 Homo sapi
2	680.4	67.5	682	2	HSMT07610	Bx485623 Homo sapi
3	677.4	67.2	742	14	CB957562	AGENCOURT
4	667	66.2	677	2	HSMT075890	Bx485703 Homo sapi

5	655	65.0	677	2	HSW0756629	BX4855442	Homo sapi
6	655	65.0	677	2	HSW076867	BX4656680	Homo sapi
7	654.6	64.9	675	2	HSW076755	BX466566	Homo sapi
8	647	64.2	675	2	HSW076748	BX466561	Homo sapi
9	641.4	63.6	665	2	HSW075590	BX4854503	Homo sapi
10	640.4	63.5	678	2	HSW077932	BX487745	Homo sapi
11	633.4	62.8	647	2	HSW077857	BX487670	Homo sapi
12	614.2	60.9	672	2	HSW074459	BX444273	Homo sapi
13	605	60.0	658	2	HSW075827	BX4555440	Homo sapi
14	603.4	59.9	618	2	HSW074630	BX454444	Homo sapi
15	585.4	58.1	610	2	HSW075337	BX485150	Homo sapi
16	562	55.8	573	2	HSW076631	BX456444	Homo sapi
17	549.4	54.5	572	2	HSW076126	BX455939	Homo sapi
18	541.8	53.8	572	2	HSW074549	BX443633	Homo sapi
19	519	51.5	531	2	HSW075965	BX466778	Homo sapi
20	516.8	51.3	531	2	HSW076729	BX466542	Homo sapi
21	490.6	48.7	542	2	HSW081001	BX509214	Homo sapi
22	483.8	48.0	498	2	HSW076978	BX466791	Homo sapi
23	483.8	48.0	503	2	HSW076402	BX466215	Homo sapi
24	476	47.2	491	2	HSW076125	BX455938	Homo sapi
25	467.8	46.4	483	2	HSW075308	BX465121	Homo sapi
26	451	44.7	514	2	HSW075124	BX44937	Homo sapi
27	433.6	43.0	449	2	HSW076457	BX456270	Homo sapi
28	403.8	40.1	504	2	HSW076054	BX465867	Homo sapi
29	394	39.1	405	2	HSW077483	BX467296	Homo sapi
30	299	29.7	299	2	HSW077075	BX466888	Homo sapi
31	258.2	25.6	437	2	HSW077573	BX467366	Homo sapi
32	227	22.5	227	2	HSW074843	BX444657	Homo sapi
33	215	21.3	747	14	CB9585709	CB9585709	AGENTOURT
34	178.2	17.7	682	2	HSW075684	BX465497	Homo sapi
35	153	15.2	1302	11	AKO15291	AKO15291	Mus muscu
36	133	13.2	499	10	BF544627	BF544627	UI-R-BTO-
37	131.2	13.0	492	28	AO133079	AO133079	HS 2188-A
38	131	13.0	926	14	BY714849	BY714849	BY714849
39	125.8	12.5	711	12	BM934267	UI-M-CG0D	
40	109.6	10.9	700	14	CAS10498	UI-R-FJO-	
41	109.6	10.9	754	14	CAS12401	CAS12401	UI-R-FJO-
42	109.6	10.9	756	14	CAS12995	UI-R-FJO-	
43	108	10.7	594	14	CB584404	AMGNNUC-M	
44	108	10.7	605	28	AZ640386	AM0502R21	
45	108	10.7	718	28	AZ972907	AZ972907	2M0246M24

ALIGNMENTS

RESULT 1	
MSM075873	
ID	MSM075873 standard; RNA; EST; 703 BP.

DT	09-MAY-2003 (Rel. 75, Created)
DT	09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX	
XX	
DE	Homo sapiens mRNA; EST DKFZp686C15248_r1 (from clone DKFZp686C15248)
XX	
XX	
KM	EST; expressed sequence tag.

OS Homo sapiens (human)
OC Euryarchaeota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
XX
KN
KN [1]
RP 1-703
RA Ottenaelder B., Obermaier B., Deutschenbauer S., Mewes H.W., Weill B.,
RA Amid C., Osanger A., Fobo G., Han M., Wiemann S.,
RT
RL Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL MRS, Ingoltschneider Landstr.1, D-85764 Neuherberg, GERMANY
XX

	CC	This is the 5' sequence of the clone insert
	CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
	CC	sequenced by MediGenomix (Martinsried/Germany) within the cDNA No. 61 sequence available.
	CC	This clone (DKFZ686C15248) is available at the RZPD in Berlin.
	CC	Please contact the RZPD; Ressourcenzentrum, Heubnerweg 6,
	CC	14059 Berlin-Charlottenburg; GERMANY; Email: clone@rzd.de
	XX	
	FH	Key Location/Qualifiers
	FH	
	FT	source
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	FT	/db_xref="taxon:9606"
	FT	/mol_type="mRNA"
	FT	/organism="Homo sapiens"
	FT	/clone="DKFZ686C15248"
	FT	/clone_lib="686 (synonym: hicc3). Vector pSport1_SfiI; host DH10B; sites SfiIA + SfiIB"
	FT	/dev_stage="adult"
	FT	/tissue_type="cdna-collection"
	XX	
	SQ	Sequence 703 BP; 158 A; 195 C; 151 G; 199 T; 0 other;
	Query Match	69.7%; Score 703; DB 2; Length 703;
	Best Local Similarity	100.0%; Pred. No. 1.1e-103;
	Matches 703; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	38	TCTAANAAGNAAAATATAATTATTTAAAAATACATTGCGTAATTTCTAAACAATAAATTT
Dd	1	TCTAANAAGAAGAAAATATAATTATTTAAAAATACATTGCGTAATTTCTAANAACAATAAATTT
OY	98	ATAAGTCTTAATTCATATGGGTCAATCAAATGAAGCTTCTCCTTTGGGCTGCATTGTA
Dd	61	ATAGGTAAATATCATATGAGGTCAATCAAAATGAAGCTTCTCCTTTGGGCTGCATTGTA
OY	158	TGTGTTGCTTTTGCAAGGAAGAAGGTTCCCCCTCATTTGGGAAGATGACAAATGAGAT
Dd	121	TGTGTTGCTTTTGCAAGGAAGAAGGTTCCCCCTCATTTGGGAAGATGACAAATGAGAT
OY	218	GATCACCACTWCATCATCTCTGAATATTCCTTAGCATACGAAATTTACCACCTCT
Dd	181	GATCACCACTTCATCATCTCTGAATATTCCTTAGCATACGAAATTTACCACCTCT
OY	278	CTTTATTATCGGCCAGTGAATACAGTCCCAGTTAACCTGGGAATPACTTACAGTACACA
Dd	241	CTTTATTATCGGCCAGTGAATACAGTCCCAGTTAACCTGGGAATPACTTACAGTACACA
OY	338	GGGTTAACCTTGATACCCCTGATTTCTTAATCTCTCTGATATCCCTTAATGTCTATACATC
Dd	301	GGGTTAACCTTGATACCCCTGATTTCTTAATCTCTCTGATATCCCTTAATGTCTATACATC
OY	398	CGTGGTTTTCCCTTAGTACTAGTACGTATGTAATGTTCTCTCTCCCTCAAGGGATTTCCCG
Dd	361	CGTGGTTTTCCCTTAGTACTAGTACGTATGTAATGTTCTCTCTCCCTCAAGGGATTTCCCG
OY	458	TTTGTCCCTCCTTCAAGGTTTTTTTTCAGAGCTGACAGACCCGCTGCCCCCACTAATGCA
Dd	421	TTTGTCCCTCCTTCAAGGTTTTTTTTCAGAGCTGACAGACCCGCTGCCCCCACTAATGCA
OY	518	GCTAGACCTGCTGACGCTGACACCTCTTACAGCACAACCTGTATAGACAGCTGAGCTGCTGCA
Dd	481	GCTAGACCTGCTGACGCTGACACCTCTTACAGCACAACCTGTATAGACAGCTGAGCTGCTGCA
OY	578	GGGGCCCTGTGTCAGCTGAGGCTGCTGCAAGAGGCACTGTTGAGGCTGAGGCTGCTGCA
Dd	541	GGGGCCCTGTGTCAGCTGAGGCTGCTGCAAGAGGCACTGTTGAGGCTGAGGCTGCTGCA
OY	638	GAGGCACTGTGTCAGCTGAGGCTGCTGCAAGAGGCACTGTTGAGGCTGAGGCACTGCA
Dd	601	GAGGCACTGTGTCAGCTGAGGCTGCTGCAAGAGGCACTGTTGAGGCTGAGGCACTGCA
OY	698	GAGGAACCTTACCAAGCTGAGCTGCTGTAACAGCAACCTGCTG 740

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Db      661 GAGGAACCTTCACCAGCTGAGCGCTGTACAGCCAGCCTGCTG 703

RESULT 2
ID      HSM076010 standard; RNA; EST; 682 BP.
XX      BX485923;
XX      BX485923.1
SV      09-MAY-2003 (Rel. 75, Created)
DT      09-MAY-2003 (Rel. 75, Last updated, Version 1)
DB      Homo sapiens mRNA; EST DKFP686L06248_r1 (from clone DKFP686L06248)
KW      EST; expressed sequence tag.
XX      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia
OC      Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX      [1]
RN      1-682
RP      Ottenmaier B., Obermaier B., Deutschenbauer S., Mewes H.W., Weil B.,
RA      Amdt C., Osanger A., Fobo G., Han W., Wiemann S.;
RL      Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Ingolstaedter Landster.1, D-85764 Neuberg, GERMANY
XX      This is the 5' sequence of the clone insert
CC      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC      Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC      sequenced by MediGenomix (Martinried/Germany) within the CDNA
CC      sequencing consortium of the German Genome Project.
CC      No sl sequence available.
CC      This clone (DKFP686L06248) is available at the RZPD in Berlin.
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC      14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX      XX
XX      Location/Qualifiers
FH      source
FT      1..682
          /db_xref="taxon:9606"
FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone="DKFP686L06248"
FT      /clone_1kb="686 (synonym: hicc3). Vector psport1_sfi; host
FT      DH10B; sites SfiIA & SfiIB"
FT      /dev_stage="adult"
FT      /rissue_type="CDNA-collection"
SQ      Sequence 682 BP; 141 A; 199 C; 150 G; 192 T; 0 other:
Query Match      67.5%; Score 680.4; DB 2; Length 682;
Best Local Similarity 99.9%; Pred. No. 4; se-100;
Matches 681; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      72 TGCGTATTTCTAAACAATAAATTATTTACTGTTAATATCATAGGGTCANCAATAATGA 131
Dd      1 TGCCTATTTCTAAAACAATAAATTATTTAGTGTTAATATTCATAGGTCATCAATAATGA 60
QY      132 AGCTTCCTCCTTTGGGCGCTGCATTTGATGTTCCTTTTGCAGAAGAGAAGCGTTCCCT 191
Dd      61 AGCTTCCTCCTTTGGGCGCTGCATTTGATGTTCCTTTTGCAGAAGAGAAGCGTTCCCT 120
QY      192 TCATTGTGAGATGACATGACGATGTCACCCACTTCATTCATCTCTGAATATTTCTT 251
Dd      121 TCATTGTGAGATGACATGACGATGTCACCCACTTCATTCATCTCTGAATATTTCTT 180
QY      252 ATGCCATACGGAATTNCCAACCTCCTCTTATTAATGCGCCAGTGAATACAGTCCCAGTT 311

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XX		BA485703;	
AC			
XX		BA485703.1	
SV			
XX		09-MAY-2003 (Rel. 75, Created)	
DT		09-MAY-2003 (Rel. 75, Last updated, Version 1)	
XX			
DE		Homo sapiens mRNA; EST DKFP66D09248_r1 (from clone DKFP66D09248)	
XX			
XX		EST; expressed sequence tag.	
KM			
XX		Homo sapiens (human)	
OS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia	
OC		Eutheria; Primates; Catarrhini; Homnidae; Homo.	
CC			
XX			
RN	[1]		
RP	1-677		
RA	Ottewelselder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,		
RA	Amid C., Osanger A., Pobo G., Han W., Wiemann S.;		
RT	'		
RL	Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases.		
MIS,	Ingelstaedter Landstr.1, D-85764 Neuberg, GERMANY		
CC	This is the 5' sequence of the clone insert		
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer		
CC	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;		
CC	sequenced by Medigenomix (Martinied/Germany) within the CDNA		
CC	sequencing consortium of the German Genome Project.		
CC	No al sequence available.		
CC	This clone (DKFP66D09248) is available at the RZPD in Berlin.		
CC	Please contact the RZPD: Ressourcencentrum, Heubnerweg 6,		
CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de		
XX			
FH	Key	Location/Qualifiers	
FT			
FT	source	1..677	
FT		/db_xref="taxon:9606"	
FT		/mol_type="mRNA"	
FT		/organism="Homo sapiens"	
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FT		/dev_stage="adult"	
FT		/issue_type="CDNA-collection"	
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	Best Local Similarity	100.0%; Pred. NO. 7e-98;	
	Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY			
	3 ACAGACTTAAATCAATGATCTTCCTCGTTCTCTCTAAGAAGAAAATAATTAA 62		
DB	11 ACAAGCTTAATAAACCATGATCTTCCTCGTTCTCTCTAAGAAGAAAATAATTAA 70		
QY	63 AAAATACATTCGGTAATTTCTTAAACAATAAATTATAGTGTATATTCATAGGCTCAA 122		
DB	71 AAATACATTCGGTAATTTCTTAAACAATAAATTATAGTGTATATTCATAGGCTCAA 130		
QY	123 TCAGAAATGAAGCTCTCCTTTGGGGCTGCATGTATGTGTGCTTTTGCAAGAGAAGAC 182		
DB	131 TCAAAATGAAGCTCTCCTTTGGGGCTGCATGTATGTGTGCTTTTGCAAGAGAAGAC 190		
QY	183 GGTGCCCTTATGGTAGGATGACATGACATGACATGACATGACATGACATGACATGACAT 242		
DB	191 GGTGCCCTTATGGTAGGATGACATGACATGACATGACATGACATGACATGACATGACAT 250		
QY	243 ATATTCCTTATGGTAGGATGACATGACATGACATGACATGACATGACATGACATGACAT 302		
DB	251 ATATTCCTTATGGTAGGATGACATGACATGACATGACATGACATGACATGACATGACAT 310		
QY	303 TCCCCAGTTACCCTGGGAATCTTACACTGACACAGGGTTACTTGGTATCCCTGATTC 362		

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Db      311 TCCCACTTACCTGGGAATACTTAACAAGACAGAGGTTACTTGTAATCCCGAATTTC
Oy      363 TAACTTCTCTGGAATTCCTCATGTATACACATCCGTGGTTTTCCCTTAGCTACTCACT 422
Db      371 TAACTTCTCTGGAATTCCTCATGTATACACATCCGTGGTTTTCCCTTAGCTACTCACT 430
Oy      423 TGATGTGTCCTCCCTCCCTCAGGAGGTTTTCCCCTTTGCCCTCCTTCAAGGTTTTTTT 482
Db      431 TGAATGTCTCTCTCTCTCTCTCAAGGAGGTTTTCCCCTTTGCCCTCCTTCAAGGTTTTTTT 490
Oy      483 CAGCAGCTGAGAGCACCCGCTATGCCCACTATTGACACTGAGCTCTGACGTGCACCTC 542
Db      491 CAGCAGCTGAGAGCACCCGCTATGCCCACTATTGACACTGAGCTCTGACGTGCACCTC 550
Oy      543 TTACAGCCCAACCTGTATAGCAGCTGAGCTCTGACAGGGGCCCTGTGTGACAGCTGAGCTG 602
Db      551 TTACAGCCCAACCTGTATAGCAGCTGAGCTCTGACAGGGGCCCTGTGTGACAGCTGAGCTG 610
Oy      603 CTGACAGAGGACCTGTGTGAGCTGAGCCTGTGACAGAGGACCTGTGTGAGCTGAGCTG 662
Db      611 CTGACAGAGGACCTGTGTGAGCTGAGCCTGTGACAGAGGACCTGTGTGAGCTGAGCTG 670
Oy      663 CTGCAGA 669
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Db      671 CTGCAGA 677

RESULT 5
HSM075629          strand, RNA; EST; 669 BP.
ID   HSM075629
XX    BX485442;
XX    BX485442.1
SV     BX485442.1
DT    09-MAY-2003 (Rel. 75, Created)
Dt    09-MAY-2003 (Rel. 75, Last updated, Version 1)
DE     Homo sapiens mRNA; EST DKFZp686D11247_r1 (from clone DKFZp686D11247)
KW     EST, expressed sequence tag.
OS     Homo sapiens (human)
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
NC     Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN     [1]
RP     1-669
RA     Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA     Han W., Wiemann S.;
RL     Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
RT     MIPS, Ingolstraedter Landstr.1, D-85764 Neuherberg, GERMANY
RL     xx
CC     This is the 5' sequence of the clone insert
CC     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC     Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC     sequenced by QIAGEN (Hilden/Germany) within the cDNA sequencing
CC     consortium of the German Genome Project.
CC     No sl sequence available.
CC     This clone (DKFZp686D11247) is available at the RZPD in Berlin.
CC     Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC     14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
CX     xx
FH     Key           Location/Qualifiers
FT     source       1..669
FT                /db_xref="taxon:9606"
FT                /mol_type="rRNA"
FT                /organism="Homo sapiens"
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FT                /clone_1nb="666 (synonym: hlcc3). Vector pSport1_sfi; host

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Oy 550 CACACCTGTAGAGCTGAGCCCTGTCAGAGGGCCCTGTGGAGCTGAGCCTGTGACGA 609
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Db 563 CACACCTGTAGAGCTGAGCCCTGTCAGAGGGCCCTGTGGAGCTGAGCCTGTGACGA 622
Oy 610 GGACACCTGTGAGAGCTGAGCCCTGTGTCAGAGGCACTGTGGAGCTGAGCCTGTCT 664
    |||
Db 623 GGACACCTGTGAGAGCTGAGCCCTGTGTCAGAGGCACTGTGGAGCTGAGCCTGTCT 677

RESULT 7
HSM076755
ID HSM076755 standard; RNA; EST; 675 BP.
XX AC BX486568;
XX SV BX486568.1
SV 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp686H08252_r1 (from clone DKFZp686H08252)
XX EST; expressed sequence tag.
XX KM Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
XX RA Bahr A., Lauber J., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,
XX RP Han M., Wiemann S.;
XX RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
XX RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
XX This is the 5' sequence of the clone insert
XX CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
XX CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
XX CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
XX CC consortium of the German Genome Project.
XX CC No sl sequence available.
XX CC This clone (DKFZp686H08252) is available at the RZPD in Berlin.
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
XX CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
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XX /db_xref="taxon:9606"
XX /mol_type="mRNA"
XX /organism="Homo sapiens"
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XX /clone_1ib="686 (synonym: h1cc3). Vector pSport1_sfi; host
XX DH10B; sites SfiI + SfiIB"
XX /dev_stage="adult"
XX /tissue_type="CDNA-collection"
XX SQ Sequence 675 BP; 139 A; 194 C; 150 G; 191 T; 1 other;

Query Match 64.9%; Score 654.6; DB 2; Length 675;
Best Local Similarity 99.3%; Pred. No. 7e-96; Indels 1; Gaps 1;
Matches 668; Conservative 0; Mismatches 4;

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Db 3 ACATTGCGATTATTAATAAATAATTAATAGTGTATATTAATTCATAGGCTCATCA 62
Oy 127 AATGAAGCTTCTCTTGGGCGCTGCACTGTATGTGTGTCTTTGCAAGGAAGACGGTT 186
    |||
Db 63 AATGAAGCTTCTCTTGGGCGCTGCACTGTATGTGTGTCTTTGCAAGGAAGACGGTT 122
Oy 187 CCCCTTCATTGGAGATGACATGACATGATGTCACCACTTCATCTCTGATAT 246

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Db 123 CCCCTTCATTGGAGATGACATGACATGATGTCACCACTTCATCTCTGATAT 182
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    |||
Db 183 TCCTTAATGCAATACGAATTTTACACCTCTCTTTATTAATGCGCAATGATACAGTCCC 242
Oy 307 CAGTTACCTGGAAATCTTACACTGACACAGGGTTACTTCTGATCCCTGATTTTAC 366
    |||
Db 243 CAGTTACCTGGAAATCTTACACTGACACAGGGTTACTTCTGATCCCTGATTTTAC 302
Oy 367 TTCTCTGATTTCCCTTAATGCTATACATCCGTGTTTCCCTTACCTACTGATTGAA 426
    |||
Db 303 TTCTCTGATTTCCCTTAATGCTATACATCCGTGTTTCCCTTACCTACTGATTGAA 362
Oy 427 TGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486
    |||
Db 363 TGTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 422
Oy 487 AGCTGACAGACCCGCTGCCCCACCTATTGACAGCTGACCTGCTGACCTGACCTTTAC 546
    |||
Db 423 AGCTGACAGACCCGCTGCCCCACCTATTGACAGCTGACCTGCTGACCTGACCTTTAC 482
Oy 547 AGCCACACCTGTAGACAGCTGAGCTGTCAGAGGGCCCTGTGTCAGCTGAGCTGCTGC 606
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Oy 607 AGAGGACCTGTGTGAGCTGAGCTGCTGTCAGAGGACCTGTGTCAGCTGAGCTGCTGC 666
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Oy 667 AGAGGACCTGTGTGAGCTGAGCTGCTGTCAGAGGACCTGTGTCAGCTGAGCTGCTGC 726
    |||
Db 603 AGAGGACCTGTGTGAGCTGAGCTGCTGTCAGAGGACCTGTGTCAGCTGAGCTGCTGC 662
Oy 727 AGCCAGCTGCT 739
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Db 663 AGCCAGCTGCT 675

RESULT 8
HSM076748
ID HSM076748 standard; RNA; EST; 675 BP.
XX AC BX486561;
XX SV BX486561.1
SV 09-MAY-2003 (Rel. 75, Created)
DT 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp686H02052_r1 (from clone DKFZp686H02052)
XX EST; expressed sequence tag.
XX KM Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX [1]
XX RA Bahr A., Lauber J., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,
XX RP Han M., Wiemann S.;
XX RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
XX RL MIPs, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
XX This is the 5' sequence of the clone insert
XX CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
XX CC Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
XX CC sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
XX CC consortium of the German Genome Project.
XX CC No sl sequence available.

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Oy		301	AGTCCCGAGTTACCTTGGAATATCTACGTGACAGAGGGTTACTTCGATCCTGGAT	360		
Dd		312	AGTCCCGAGTTACCTTGGAATATCTACGTGACAGAGGGTTACTTCGATCCTGGAT	371		
Oy		361	TCTAACTTCTCTGGATTCCCTATATGTCATACATCCGTGTTTTCCCTTAAGTACTCA	420		
Dd		372	TCTAACTTCTCTGGATTCCCTATATGTCATACATCCGTGTTTTCCCTTAAGTACTCA	431		
Oy		421	GTTGAAGTTCTCTCTCTCTCCCTCTTAGGGGTTTTCCGTTTGTCCCTTCCTTCAAGGTTTTT	480		
Dd		432	GTTGAAGTTCTCTCTCTCTCCCTCTTAGGGGTTTTCCGTTTGTCCCTTCCTTCAAGGTTTTT	491		
Oy		481	TTGAGCAGCTGCAGCACCCGCTGCCACCACCATTTGACGTAGAGCTGCAGCTGACCC	540		
Dd		492	TTGAGCAGCTGCAGCACCCGCTGCCACCACCATTTGACGTAGAGCTGCAGCTGACCC	551		
Oy		541	TCTTACAGCCACACCTGTAGAGCTGAGCCTGTCTGCAGGGGCCCTGTGTGACGTAGCC	600		
Dd		552	TCTTACAGCCACACCTGTAGAGCTGAGCCTGTCTGCAGGGGCCCTGTGTGACGTAGCC	611		
Oy		601	TGCTGCAGAGGACCTGTTGGAGCTGAGCCTGCTGCAGAGGACACCTGTTGACGCT	655		
Dd		612	TGCTGCAGAGGACA-CTGTTGGAGCTGAGCCTGCTGCAGAGGACACCTGTTGACGCT	665		
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XX	XX	BSX87745.1				
SV						
XX						
DT	09-MAY-2003 (Rel. 75, Created)					
DT	09-MAY-2003 (Rel. 75, Last updated, Version 1)					
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DE	Homo sapiens mRNA; EST DKFPZ666N16258_r1 (from clone DKFPZ666N16258)					
XX						
KW	EST; expressed sequence tag.					
XX						
OS	Homo sapiens (human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;					
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.					
XX						
RN	[1]					
RP	1-678					
RA	Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,					
RA	Han M., Wiemann S.;					
RT						
RL	Submitted (07-MAY-2003) to the EMBL/GenBank/DDJ databases.					
RL	MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY					
XX						
CC	This is the 5' sequence of the clone insert					
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer					
CC	Research Center (DKFZ), Email s.wiemann@dkz-heidelberg.de;					
CC	sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing					
CC	consortium of the German Genome Project.					
CC	No sl sequence available.					
CC	This clone (DKFPZ666N16258) is available at the RZPD in Berlin.					
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,					
CC	14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de					
PH						
Key	Location/Qualifiers					
FT	source					
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FT	/mol_type="mRNA"					
FT	/organism="Homo sapiens"					
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FT	/tissue_type="cDNA-collection"					

XX	Sequence	678 BP; 158 A; 180 C; 132 G; 207 T; 1 other;
XX	Query Match	63.5%; Score 640.4; DB 2; Length 678;
XX	Best Local Similarity	99.5%; Pred. No. 1.4e-93;
XX	Matches	652; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY	1 AGACAGCTAAAAAGCCATGTATTCCTTCCTGTTCTCTCTAAAGAAAGAAAAATATATAT	60
DB	25 AGACAGCTAAAAAGCCATGTATTCCTTCCTGTTCTCTAAAGAAAGAAAAATATATAT	84
QY	61 TAAAAATACATGGCGATTTTCTTAAACAATAAATTATAGTTATATTCATAGGCTC	120
DB	85 TAAAAATACATGGCGATTTTCTTAAACAATAAATTATAGTTATATTCATAGGCTC	144
QY	121 AATCAAAATGAAGCTTCTCCTTTGGGCTGTCATTTGATGTTGCTTTTGCAAGAAAG	180
DB	145 AATCAAAATGAAGCTTCTCCTTTGGGCTGTCATTTGATGTTGCTTTTGCAAGAAAG	204
QY	181 ACGGTTCCCTTCATCTGGTAGAGATACATAAGAGAGGACCCCTCATCCATCTCT	240
DB	205 ACGGTTCCCTTCATCTGGTAGAGATACATAAGAGAGGACCCCTCATCCATCTCT	264
QY	241 GAATATTCCTTATGAGCATACGAATTTTACCACTCCTCTTATATATGCGCCAGTAAATAC	300
DB	265 GAATATTCCTTATGAGCATACGAATTTTACCACTCCTCTTATATATGCGCCAGTAAATAC	324
QY	301 AGTCCCAAGTTACCTGAGAAATCTTACACTGACACAGAGGTTACCTTGATCCTGGAT	360
DB	325 AGTCCCAAGTTACCTGAGAAATCTTACACTGACACAGAGGTTACCTTGATCCTGGAT	384
QY	361 TCTAATCTTCCTGAGATATCCCTCATGTCATCATCCGATGTTTCCCTTAGCTATCTCA	420
DB	385 TCTAATCTTCCTGAGATATCCCTCATGTCATCATCCGATGTTTCCCTTAGCTATCTCA	444
QY	421 GTTGAATGTTCTCTCTCTCCCTCTAGAGGGTTCCCGTTTGTCCTCTTCAAGGTTT	480
DB	445 GTTGAATGTTCTCTCTCTCCCTCTAGAGGGTTCCCGTTTGTCCTCTTCAAGGTTT	504
QY	481 TTTCAGCAGCTGACGACACCCGCTCCACCCTATTTGACGCTGAGCCTGTCAGCTGCACC	540
DB	505 TTTCAGCAGCTGACGACACCCGCTCCACCCTATTTGACGCTGAGCCTGTCAGCTGCACC	564
QY	541 TCTTACACCAACACTGTAGACAGCTGCTGTCGACAGGAGCCCTGTGTGACGTGAGCC	600
DB	565 TCTTACACCAACACTGTAGACAGCTGCTGTCGACAGGAGCCCTGTGTGACGTGAGCC	623
QY	601 TGCTGACAGAGGACCTGTGAGCTGAGCTGTGTCGACAGGACCTGTGTGACGT	655
DB	624 TGCTGACAGAGGACCTGTGAGCTGAGCTGTGTCGACAGGACCTGTGTGACGT	678
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XX	ID HSM077857	standard; RNA; EST; 647 BP.
XX	AC BX487670;	
XX	XX BX487670.1	
SV	XX BX487670.1	
XX	XX	
XX	09-MAY-2003 (Rel. 75, Created)	
DT	09-MAY-2003 (Rel. 75, Last updated, Version 1)	
XX	XX	
DE	Homo sapiens mRNA; EST DKFP686G13258_r1 (from clone DKFP686G13258)	
XX	XX	
XX	EST; expressed sequence tag.	
XX	Homo sapiens (human)	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;	
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.	
XX	[1]	
RP	1-647	

RA	Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RT	Han M., Wiemann S.;
RL	; Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases.
RR	MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY
XX	
CC	This is the 5' sequence of the clone insert
CC	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC	Research Center (DKFZ); Email s.wiemann@dkfz-heldelberg.de;
CC	sequenced by QIAGEN (Hilden/Germany) within the cDNA sequencing
CC	consortium of the German Genome Project.
CC	No sl sequence available.
CC	This clone (DKFZ686613258) is available at the RZPD in Berlin.
CC	Please contact the RZPD, Ressourcenzentrum, Heubnerweg 6,
CC	14059 Berlin-Charlottenburg, Germany; Email: clonewrzd.de
XX	
FH	Key Location/Qualifiers
FT	
FT	Source
FT	1..647
FT	/db_xref="taxon:9606"
FT	/mol_type="mRNA"
FT	/organism="Homo sapiens"
FT	/clone="DKFZ686613258"
FT	/clone_lib="686 (synonym: hlc63). Vector pSport1_Sfi; host
FT	DHIOB, Sites SfiI + SfiIB"
FT	/dev_stage="adult"
FT	/tissue_type="CDNA-collection"
XX	
SQ	Sequence 647 BP; 148 A; 174 C; 128 G; 197 T; 0 other;
Query Match	62.8%; Score 633.4; DB 2; Length 647;
Best Local Similarity	99.8%; Pred. No. 1.9e-92;
Matches 634; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 AGACAGACTAAAAAAAGCATTGATCTTCCTCGTTAATAAAGAAGAAAATTAAT 60
DB	13 AGACAGACTAAAAAAAGCATTGATCTTCCTCGTTAATAAAGAAGAAAATTAAT 72
OY	61 TAAATAATCATGCGTATTTTCTAATAACAATAATTATAGTGTAATATTCATAGGGTC 120
DB	73 TAAATAATCATGCGTATTTTCTAATAACAATAATTATAGTGTAATATTCATAGGGTC 132
OY	121 AATCAAAATGAAGCTTCTCCTTTGGGCGTCATTGTATGTGTGCTTTTGCAGGAAGAAG 180
DB	133 AATCAAAATGAAGCTTCTCCTTTGGGCGTCATTGTATGTGTGCTTTTGCAGGAAGAAG 192
OY	181 ACGGTCCCCCTTCAATGGTGAAGATGACATACATACATGATCCATTCCTCT 240
DB	193 ACGGTCCCCCTTCAATGGTGAAGATGACATACATACATGATCCATTCCTCT 252
OY	241 GAATATTCCTTATGSCATACGGAATTTTACACCTCTCTTATATAGGCCAGTAAATAC 300
DB	253 GAATATTCCTTATGSCATACGGAATTTTACACCTCTCTTATATAGGCCAGTAAATAC 312
OY	301 AGTCCCAGTTAACCTGTGGAATATCTTACATGACACAGGGTTACCTGTATCCCTGANT 360
DB	313 AGTCCCAGTTAACCTGTGGAATATCTTACATGACACAGGGTTACCTGTATCCCTGANT 372
OY	361 TCATACTTCTCTGTGATTCCTCTAATGTCTATACATCCGTGTGTTTTCCCTTAGCTACTCA 420
DB	373 TCATACTTCTCTGTGATTCCTCTAATGTCTATACATCCGTGTGTTTTCCCTTAGCTACTCA 432
OY	421 GTTGAATGTCTCTCTCCCTCTCAGGGGGTTTCCCGTTGTCCCTCTCAAGGTTTTT 480
DB	433 GTTGAATGTCTCTCTCCCTCTCAGGGGGTTTCCCGTTGTGTCCCTCTCAAGGTTTTT 492
OY	481 TTCAGACCTGACAGACCCTGCTCCCACTATTCAGCTGAAGCTGTGACCTGACAC 540
DB	493 TTCAGACCTGACAGACCCTGCTCCCACTATTCAGCTGAAGCTGTGACCTGACAC 552
OY	541 TCTTACAGCACACCTGTACAGCTGAGCTGTGCTGACGGGGCCCTGTTCAGCTGAGGC 600
DB	553 TCTTACAGCACACCTGTACAGCTGAGCTGTGCTGACGGGGCCCTGTTCAGCTGAGGC 612

[illegible]


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OY 181 ACGCTTCCCTTCATTTGGTGGAGATGACATGACGATGTCACCCACTTCATCCATCTCT 240
DB 193 ACGGTTCCTTCATTTGGTGGAGATGACATGACGATGTCACCCACTTCATCCATCTCT 252
OY 241 GAATATTCCTTATGAGCATATGAGATTTTACACCTCTCTTTATTTATCCGCCAGTAATAC 300
DB 253 GAATATTCCTTATGAGCATATGAGATTTTACACCTCTCTTTATTTATCCGCCAGTAATAC 312
OY 301 AGTCCCAAGTATACCTCGGAGATATTTACATGACACAGGGTTTACCTTGATCCCTGAT 360
DB 313 AGTCCCAAGTATACCTCGGAGATATTTACATGACACAGGGTTTACCTTGATCCCTGAT 372
OY 361 TCTAATCTCTCTGATATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 373 TCTAATCTCTCTGATATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 432
OY 421 GTTGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 433 GTTGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 492
OY 481 TTACAGCAGCTGAGACACCCGCTGCTCCCACTTATGACAGCTGAGCTGCTGACCTGAC 540
DB 493 TTACAGCAGCTGAGACACCCGCTGCTCCCACTTATGACAGCTGAGCTGCTGACCTGAC 552
OY 541 TCTTACAGCAGCAGCTGAGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 600
DB 553 TCTTACAGCAGCAGCTGAGACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 612
OY 601 TGCTGACAGAGCA-CCTGTTGAGAGCTGAG-CCTGCTGACAGAGCA-CCTGTTGAGAGCTG 657
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RESULT 13
HSM075827 standard; RNA; EST; 658 BP.

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XX HSM075827 standard; RNA; EST; 658 BP.
XX BX485640;
XX BX485640.1
XX 09-MAY-2003 (Rel. 75, Created)
XX 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp686P12247_r1 (from clone DKFZp686P12247)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX 1-658
XX Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fodor G.,
XX Han W., Wiemann S.;
XX Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.
XX MIPB, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
XX
XX This is the 5' sequence of the clone insert
XX Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
XX Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
XX sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
XX consortium of the German Genome Project.
XX No 31 sequence available.
XX This clone (DKFZp686P12247) is available at the RZPD in Berlin.
XX Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6,
XX 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
XX Key Location/Qualifiers
XX source 1. 658

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FT /db xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp686P12247"
FT /clone_id="686 (synonym: h1cc3). Vector pSport1_Sfi; host
FT DH10B; sites SfiI + SfiIIB"
FT /dev stage="adult"
FT /tissue_type="cDNA-collection"
SQ
Sequence 658 BP; 159 A; 173 C; 124 G; 202 T; 0 other;
Query Match 60.0%; Score 605; DB 2; Length 658;
Best Local Similarity 100.0%; Pred. No. 7e-88;
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 AGACAGACTAAAAAGCCATGATTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
DB 54 AGACAGACTAAAAAGCCATGATTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 113
OY 61 TAAAAATGATTTGGTATTTCTTAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
DB 114 TAAAAATGATTTGGTATTTCTTAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 173
OY 121 AATCAAAATGAAGCTTCTCTTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 174 AATCAAAATGAAGCTTCTCTTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 233
OY 181 ACGGTTCCCTTCATTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 234 ACGGTTCCCTTCATTTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 293
OY 241 GAATATTCCTTATGAGCATATGAGATTTTACACCTCTCTTATTAATGATGATGATGATGATGATGATGATGAT 300
DB 294 GAATATTCCTTATGAGCATATGAGATTTTACACCTCTCTTATTAATGATGATGATGATGATGATGATGATGAT 353
OY 301 AGTCCCAAGTATACCTCGGAGATATTTACACTGACACAGGGTTTACCTTGATCCCTGAT 360
DB 354 AGTCCCAAGTATACCTCGGAGATATTTACACTGACACAGGGTTTACCTTGATCCCTGAT 413
OY 361 TCTAATCTCTCTGATTTCCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 414 TCTAATCTCTCTGATTTCCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 473
OY 421 GTTGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 474 GTTGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 533
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DB 534 TTACAGCAGCTGAGACACCCGCTGCTCCCACTTATGACAGCTGAGCTGCTGACCTGAC 593
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OY 601 TGCTG 605
DB 654 TGCTG 658

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RESULT 14
HSM074630 standard; RNA; EST; 618 BP.

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XX HSM074630 standard; RNA; EST; 618 BP.
XX BX484444;
XX BX484444.1
XX 09-MAY-2003 (Rel. 75, Created)
XX 09-MAY-2003 (Rel. 75, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp686A01243_r1 (from clone DKFZp686A01243)
XX

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EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RN 1-618

RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.

RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY

XX This is the 5' sequence of the clone insert

CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

CC sequenced by Qigen (Hilden/Germany) within the CDNA sequencing consortium of the German Genome Project.

CC No sl sequence available.

CC This clone (DKFZp686A01243) is available at the RZPD in Berlin.

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source

FT 1..618

FT /db_xref="taxon:9606"

FT /mol_type="mRNA"

FT /organism="Homo sapiens"

FT /clone_id="DKFZp686A01243"

FT /clone_lib="686 (synonym: hlcc3). Vector pSPORT1_Sfi; host DH10B; sites SfiI + SfiIB"

FT /dev_stage="adult"

FT /issue_type="CDNA-collection"

XX Sequence 618 BP; 143 A; 166 C; 118 G; 191 T; 0 other;

SO Query Match 59.8%; Score 603.4; DB 2; Length 618; Best Local Similarity 99.8%; Pred. No. 1.3e-87; Matches 604; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGACAGCTAAAGAGCATATCTTCTGCTCTCTAAAGAGAAATATATTT 60

DB 14 AGACAGCTAAAGAGCATATCTTCTGCTCTCTAAAGAGAAATATATTT 73

QY 61 TAAATAATATGCTATCTTCTAAAGAAATATATATATATATATATATAT 120

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QY 121 AATCAAAATGAGGCTTCTCTTGGGCTGCAATGATGTTGCTTTGCAAGAAAG 180

DB 134 AATCAAAATGAGGCTTCTCTTGGGCTGCAATGATGTTGCTTTGCAAGAAAG 193

QY 181 ACGGTTCCCTTCAATGTTGAGATGACATGACATGACATGACATGACATG 240

DB 194 ACGGTTCCCTTCAATGTTGAGATGACATGACATGACATGACATGACATG 253

QY 241 GAATATTCCTTATGAGCATAGGAAATTTACACCTCTTATATATGCGCCAGTAATAC 300

DB 254 GAATATTCCTTATGAGCATAGGAAATTTACACCTCTTATATATGCGCCAGTAATAC 313

QY 301 AGTCCAGTTACCTGGAATCTTACCTGACAGAGGTTACCTTGATCCCTGAT 360

DB 314 AGTCCAGTTACCTGGAATCTTACCTGACAGAGGTTACCTTGATCCCTGAT 373

QY 361 TCTAATCTTCTGATGATCCCTTATGATGATGATGATGATGATGATGATG 420

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QY 421 GTTAATGTTCT 480

DB 434 GTTAATGTTCT 493

QY 481 TTACAGAGCTGACAGACCCCGCTGCCACCTATTTGAGTGAAGCTGCTGACGAC 540

DB 494 TTACAGAGCTGACAGACCCCGCTGCCACCTATTTGAGTGAAGCTGCTGACGAC 553

QY 541 TCTTACAGCAGACCTGTATGACAGTGAAGGCGCCCTGTTGACGCTGAGCC 600

DB 554 TCTTACAGCAGACCTGTATGACAGTGAAGGCGCCCTGTTGACGCTGAGCC 613

QY 601 TGCTG 605

DB 614 TGCTG 618

RESULT 15

HS075337 standard; RNA; EST; 610 BP.

XX HSM075337

XX BX485150;

XX BX485150.1

SV 09-MAY-2003 (Rel. 75, Created)

XX 09-MAY-2003 (Rel. 75, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp686A12246_r1 (from clone DKFZp686A12246)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RN 1-610

RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

RT Submitted (07-MAY-2003) to the EMBL/GenBank/DBJ databases.

RL MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY

XX This is the 5' sequence of the clone insert

CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

CC sequenced by BWFZ (Biomedical Research Center at the Heinrich-Heine-University, Dueseldorf/Germany) within the CDNA sequencing consortium of the German Genome Project.

CC No sl sequence available.

CC This clone (DKFZp686A12246) is available at the RZPD in Berlin.

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source

FT 1..610

FT /db_xref="taxon:9606"

FT /mol_type="mRNA"

FT /organism="Homo sapiens"

FT /clone_id="DKFZp686A12246"

FT /clone_lib="686 (synonym: hlcc3). Vector pSPORT1_Sfi; host DH10B; sites SfiI + SfiIB"

FT /dev_stage="adult"

FT /issue_type="CDNA-collection"

XX Sequence 610 BP; 143 A; 164 C; 115 G; 188 T; 0 other;

SO Query Match 58.1%; Score 585.4; DB 2; Length 610; Best Local Similarity 99.8%; Pred. No. 1e-84; Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 AAAAGCAGATATCTTCTGTTCTCTAAAGAGAAATATATATATATATATAT 70

DB 24 AAAAGCAGATATCTTCTGTTCTCTAAAGAGAAATATATATATATATATAT 83

OY 71 TTGGATTTTCTAAACATTAATTATAGCTTAATATTCATRGGGTCAATCAAAATG 130
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DB 84 TTGGATTTTCTAAACATTAATTATAGCTTAATATTCATRGGGTCAATCAAAATG 143
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OY 131 AAGCTTCCTTTGGGCGCTGATGTATGTGTGCTTTGCAAGGAAGAGAGGTTCCCG 190
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DB 144 AAGCTTCCTTTGGGCGCTGATGTATGTGTGCTTTGCAAGGAAGAGAGGTTCCCG 203
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OY 191 TTCAATTGGTGAGATGACATGACGATGTGACCCACTTCATCCATCTGTGAATATTCCT 250
|||
DB 204 TTCAATTGGTGAGATGACATGACGATGTGACCCACTTCATCCATCTGTGAATATTCCT 263
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OY 251 TATGGCATACGGAATTTACCACTCTCTTTATATGCGCCAGTGAATACAGTCCCGAGT 310
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DB 264 TATGGCATACGGAATTTACCACTCTCTTTATATGCGCCAGTGAATACAGTCCCGAGT 323
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OY 311 TACCCTGGGAATPACTTACACTGACACAGGGTTACCTGTATCCCTGATTCCTTAATCTT 370
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DB 324 TACCCTGGGAATPACTTACACTGACACAGGGTTACCTGTATCCCTGATTCCTTAATCTT 383
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OY 371 CCTGGATTCCTTATGTCTATCAATCCGTGTGTTTCCCTTAGCTACTCAGTTGATGTT 430
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DB 384 CCTGGATTCCTTATGTCTATCAATCCGTGTGTTTCCCTTAGCTACTCAGTTGATGTT 443
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OY 431 CCTCTCTCCCTCTAGGGGTTTCCGTTTGTCCCTCTCAAGGTTTTTTTCAGAGCT 490
|||
DB 444 CCTCTCTCCCTCTAGGGGTTTCCGTTTGTCCCTCTCAAGGTTTTTTTCAGAGCT 503
|||
OY 491 GCAGACCCGCTGCCCCCACTATTGACGTAGCGTGCAGCTGCACCTTTACAGCC 550
|||
DB 504 GCAGACCCGCTGCCCCCACTATTGACGTAGCGTGCAGCTGCACCTTTACAGCC 563
|||
OY 551 ACACCTGTAGCAGTGAAGCTGTGCAAGGGGCCCTGTGCACTGA 597
|||
DB 564 ACACCTGTAGCAGTGAAGCTGTGCAAGGGGCCCTGTGCACTGA 610
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Job time : 2135 secs